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Sequence:

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Sequence 28, Application US/10054536;
Sequence 28, Application US/10054536;
Publication No. US20030162248A1
GENERAL INFORMATION:
APPLICANT: WARAMIYA, No. US20030162248A1utaka
TITLE OF INVENTION: RECOMBINANT HUMAN MANNAN-BINDING PROTEINS AND PROCESS;
TITLE OF INVENTION: FOR PRODUCING THE SAME
TITLE OF INVENTION: POR PRODUCING THE SAME
TITLE OF INVENTION: POR PRODUCING THE SAME
CURRENT APPLICATION NUMBER: US/10/054,536
CURRENT FILING DATE: 2002-0.23
PRIOR FILING DATE: 1998-07-23
PRIOR PILING DATE: 1998-01-23
PRIOR FILING DATE: 1998-01-23
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 28
LENGTH: 248
                                                                   Sequence 1, Appli
Sequence 1, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 473, Appli
Sequence 473, Appli
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Sequence 357, Appli
Sequence 357
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Sequence 357,
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Sequence 357,
US-10-054-536-28
US-10-388-322-1
US-10-3429-160-58
US-09-971-475-1
US-10-312-829-9
US-10-007-408-1
US-10-312-829-7
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US-10-336-603A-100
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US-09-925-302-473

US-09-989-722-357

US-09-989-723-357

US-09-989-727-357

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US-09-990-562-357
US-09-990-711-357
US-09-990-711-357
US-09-990-711-357
US-09-990-711-357
US-09-990-711-357
US-09-990-71357
       ORGANISM: Homo sapiens
     Alignment Scores
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-TRANS=human40.cdi -LIST=45 -DOCALIGN=20 -THR SCORE=pct -HEAPSIZE=500 -MINLEN=0
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-THR MIN=0 -ALIGN=15 -MOMP -LARGEQUERY -NGG SCORE=0 -MIT -DSPBLOCK=100
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                                                                                                                                                                                 June 18, 2004, 21:02:52; Search time 49 Seconds (without alignments) 8607.685 Million cell updates/sec
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1. /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2. /cgn2_6/ptodata/2/pubpaa/PCT NRW PUB.pep:*

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18. /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

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18. /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                   protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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seq length: 200000000
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Jatabase

No.

Result

Minimum DB Maximum DB

us-10-054-536-2.rapb

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Matches:
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Publication No. US20040023276A1
GENERAL INFORMATION:
                                        1.03e-110
1321.00
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Best Local Similarity:
Query Match:
DB:
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300 100 360 120 420

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480 160 540 200

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; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-971-475-1
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Best Local Similarity:
Query Match:
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Pred. No.:
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US-09-971-475-1
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                                                                                                                                                                                                                                                                     CCAGGCATCAACGGCTTCCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAGGGG
APPLICANT: Ward, Teresa R
APPLICANT: Mao, Mao
APPLICANT: Linsley, Peter S
APPLICANT: Linsley, Peter S
APPLICANT: Linsley, Peter S
TITLE OF INVENTION: LINR Ligand Induced Genes and Proteins
FILE REFERENCE: RS0200
CURRENT APPLICATION NUMBER: US/10/429,160
CURRENT FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: US 60/377,714
PRIOR APPLICATION NUMBER: US 60/377,714
SPRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 111
SOFTWARE: Patentin version 3.1
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                       LENGTH: 248
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                      Score:
Percent Similarity:
Best Local Similarity:
Query Match:
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Pred. No.:
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US-10-429-160-58
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Matches:
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Mismatches:
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                                                                                                                                                                GENERAL INFORMATION:
GENERAL INFORMATION:
FULE REPERENCY:
ALCIANCE: ADT 306
FULE REFERENCE: ADT 306
CURRENT APPLICATION NUMBER: US/09/971,475
CURRENT FILING DATE: 2001-10-04
PRIOR PELING DATE: 1999-12-21
PRIOR FILING DATE: 1999-12-21
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1998-08-19
PRIOR FILING DATE: 1997-08-21
NUMBER: OF SEQ ID NOS: 2
SEQ ID NO 1
                                                         241 LeuAlaValCysGluPheProlle
                                             721 CIGGCCGICIGIGAGIICCCIAIC
                                                                                                                          ; Sequence 1, Application US/09971475; Publication No. US20020086817A1; GENERAL INFORMATION:
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	ATGGCCAGTGGAATGACGTCCCTGCTCCAGTCCAGTCCA	STATE: ILITIOAS  COUNTRY: United States of America  COMPUTER: E0606-402  COMPUTER: PROADBLE FOODY disk  MEDIUM TYPE: Floppy disk  COMPUTER: ILIM FOCOMPATE: PC-DOS/MS-DOS  SCHWARE: Patentin Release #1.0, Version #1.30  CURRENT APPLICATION NUMBER: US/10/007, 408  FILING DATE: 08-No. US2020168627A1-2001  FILING DATE: 08-No. US2020168627A1-2001  FILING DATE: 08-No. US2020168627A1-2001  FILING DATE: 08-No. US2020168627A1-2001  APPLICATION NUMBER: PCT/1P95/02035  APPLICATION NUMBER: PCT/1P95/02035  ATTORNEY/AGENT INFORMATION:  REPERENCE/DOCKET NUMBER: 19036/34546  TELECOMMUNICATION INFORMATION:  REPERENCE/DOCKET NUMBER: 19036/34546  TELEPHONE: (312) 474-6300  TELEPHO
Qy         541 GAAGCCTTCCTGGGCATCATGAGAAGACAGAAGGACGTTTGTGGATCTGACAGA           b         161 GlualaPheLeuGly11eThrAspGluLySThrGluGlyGlnPheValAspLeuThrGly           b         161 GlualaPheLeuGly11eThrAspGluLySThrGluGlyGlnPheValAspLeuThrGly           Qy         601 AATAGACTGACCTACACAAACTGGACGAGGAGTGACCCAACAATGCTGGTCTGATGAA           b         181 ASTAGTGTATTGCTACTGAAAATTGAGGGGTGAACCCAACAATGGTGGTTCTGATGAA           Qy         661 GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCTGCTCCACCTCCCACT           10         1	SULT 5  SQUENCE 9, Application US/10312829  SQUENCE 9, Application US/10312829  STATE OF UNFORMATION:  FILE OF INVENTION: Peptides with An FILE REFERENCE: 10738-31  CURRENT APPLICATION NUMBER: US/10/31  CURRENT FILING DATE: 2003-08-04  PRIOR APPLICATION NUMBER: PCT/US01/2  PRIOR APPLICATION NUMBER: COT/US01/2  PRIOR APPLICATION NUMBER: US 60/215, PRIOR PILING DATE: 2000-06-30  NUMBER OF SEQ ID NOS: 17  SOFTWARE: PATENTING DATE: 2000-06-30  NUMBER OF SEQ ID NOS: 17  SOFTWARE: PATENTING DATE: 2000-06-30  NUMBER OF SEQ ID NOS: 17  SEQ ID NO 9  LENGTH: 375  TYPE: PRT  ORGANISM: Homo sapiens	### Adjustment Scores:    Pred. No.:

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Percent Similarity: 56.77% Conservative: 39 Best Local Similarity: 39.74% Mismatches: 74 Query Match: 32.42% Indels: 25	; TYPE: PKT ; ORGANISM: Rat US-10-312-829-7
caps: )-007-408-1 (1-351)	Alignment Scores: Pred. No.:
CTCCAGGCATC	Score: Percent Similarity: Best Local Similarity Query Match:
	DB: US-10-054-536-2 (1-747
143 GlyalabroGlyGluThrGlyAlaProGlyArgAlaGlyValThrGlyProSerGlyAla 162	Qy 10 TITCCATC
226 TIGGGGCCICCAGGAAICCAGGGCCTICIGGGTCACCAGGACCAAAGGGCCAAAAGGA 285	
GACCCTGGAAAAAGTCCGGATGGTGATAGTAGCTGGCTGGCTGCC	70
	Db 24 ThrLeuSe
328TCAGAAAGAAAAGTCTCTGCAAACAGAAATGGCACGTATC 366	
203 GlnArgValThrIleLeuAspGlyHisLeuArgArgPhedlnAsnAlaPheSerGlnTyr 222	Qy 181 GAACCAGG
367 AAAAAGTGGCTGACCTCTCTCTGGGAAACAAGTTGGGAACAACTTCTTCTCACAAT 426         :::	
	Qy 190
;:: ;::::       ;:: 243 GlyAlaValLysSerTyrSerAspAlaGluGInLeuCysArgGluAlaLysGlyGlnLeu 262	208
487 GCCACCCCCAGAATGCTGCAGAATGGAGCCATTCAGAATCTCATCAAG 537    :::      :::	104
GAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGGCAGTTTGTGGATCTGACA	220
:::    :::    :::	Ov 274 GGCCAAAI
GGAAATAGACTGACCTACACAACTGGAACGAGGAGCGAACCCAACAATGCTGGT	144
GlyGluIleLeuValTyrSerAsnTrpAlaAspGlyGluProAsnAsnSerAspGluGLY	Oy 309
652 TCTGATGAAGATTGTGTATTGCTACTGAAAATGGCCAGT65AATGACGTCCCTGCTCC /11 322 CTGTGATGAAGATTGTGTATTGCTACAAAATGGCCAGT65AATGACGTCCCCTGCTCC /11 322 CTGTGATGAAGATGTTGTATTAAAAAAAAAAAAAAAAAA	Db 164 LysGlyG
ACTICIONATION GRACIONATION AND THE STATE OF	308
LysGlnLeuLeuVallleCysGluPhe 35	Db 184 ProAlaG
RESULT 7 US-10-312-829-7	
Sequence 7, Application US/10312829 Publication No. US20040037781A1	Qy 316 AGCCTGG
	Db 224 AlaAlaL
tadiic ana Aicimiciobiai Fioperise	Qy 367
CURRENT APPLICATION NUMBER: US/10/312,829 CURRENT FILING DATE: 2003-08-04	Db 244 PheSerA
ALCA AFFILMED DATE: 2001-06-29 RICR FILING DATE: 2001-06-29 RICR APPLICATION UNMBER 105 60/215,313	Oy 415 TTCCTGA
PKIOK FILING DAIS: 2000-08-30 NUMBER OF SEQ ID NOS: 17 SOFTWARE PatentIn version 3.1	475
SEQ ID NO 7 LENGTH: 374	Db 284 GlyGlyG

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LeuArgGlnGlnMetGluAlaLeuAsnGlyLysLeuGlnArgLeuGluAlaAla 243
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erGlnArgSerIleThrAsnThrCysThrLeuValLeuCysSerProThrGlu 43
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|serMetLeuValLeuLeuValGlnProLeuGlyAspLeuGlyAlaGluMetLys
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Length:
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RESULT 9

US-10-312-829-4

i Sequence 4, Application US/10312829

i Sequence 4, Application No. US20040037781A1

i GENERAL INFORMATION:

i APPLICANT: MCCORMACK, Francis X

TITLE OF INVENTION: Peptides with Antioxidant and Antimicrobial Properties

FILE REFERENCE: 10738-31

i CURRENT FAPLICATION NUMBER: US/10/312,829

CURRENT FILING DATE: 2003-0824

i PRIOR APPLICATION NUMBER: PCT/US01/21226

i PRIOR APPLICATION NUMBER: US 60/215,313

PRIOR FILING DATE: 2000-06-30

i NUMBER OF SEQ ID NOS: 17

i SEQ ID NO 4

i ERNGTH: 248
91 ProGlyGluArg-----GlyLeuProGlyPheProAlaTyrLeuAspGluGluLeuGln 108
                                                                        109 ThrGluLeuTyrGluIleLysHisGlnIleLeuGlnThrMetGlyValLeuSerLeuGln 128
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169 GluGluAsnGluAlaileAlaSerIleAlaLysLysTyrAsnAsnTyrValTyrLeuGly 188
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                                                                                                                                       129 GlySerMetLeuSerValGlyAspLysValPheSerThrAsnGlyGlnSerValAsnPhe
                                                                                                                                                                                       445 GAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCCCCCAGGAATGCT
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                                                                                                                394 ------AAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTT
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                                     349 ACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCTCTGGGC
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Best Local Similarity:
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248 Phe 248
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US-10-312-829-4
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US-10-312-829-12

Sequence 12, Application US/10312829

Publication No. US20040037781A1

GENERAL INFORMATION:

TITLE OF INVENTY: MCCOrmack, Francis X

TITLE OF INVENTION: Peptides with Antioxidant and Antimicrobial Properties

CURRENT PAPLICATION NUMBER: US10/312,829

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: PCT/US01/21226

PRIOR APPLICATION NUMBER: US 60/215,313

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12
                                                                                          645
                                                                                                            GCTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCC 705
                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: antioxidant peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAGGGG 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGICCCTGTTTCCATCACTCCCTCTCTCTCTGAGTATGGTGGCAGCGTCTTACTCA 60
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ProProGlyPro------MetGlyProProGlyGlyMetProGlyLeuPro 70
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                                 304 ThralaHisSerLysalaAlaPheLeuSerMetThrAspValGlyThrGluGlyLysPhe
           -----AAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTT
                                                                                  GTGGATCTGACAGGAAATAGACTGACCTACAAACTGGAACGAGGGTGAACCCAACAAT
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ORGANISM: Artificial Sequence
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Sequence 100, Application US/10336603A
Publication No. US20040072997A1
GENERAL INFORMATION:
APPLICANT: Alsobrook et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOI FILE REPERENCE: 2.1402-533A
CURRENT APPLICATION NUMBER: US/10/336,603A
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Best Local Similarity:
Query Match:
DB:
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TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD FILE REFERENCE: 21402-253A
CURRENT APPLICATION NUMBER: US/10/336,603A
CURRENT FILING DATE: 2003-01-03
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR APPLICATION NUMBER: 09/746,491
PRIOR PILING DATE: 2000-12-20
PRIOR PELING DATE: 2001-10-26
PRIOR PELING DATE: 2001-10-26
PRIOR PELING DATE: 2001-10-26
PRIOR FILING DATE: 2001-10-26
PRIOR PRIO
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|GluGluAsnGluAlaIleAlaSerPheValLysLysTyrAsnThrTyrAlaTyrValGly 188
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                            GGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAAGGGGGAACCAGGCCAAGGGCTCAGA 201
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US-10-336-603A-96
Sequence 96, Application US/10336603A
Publication No. US20040072997A1
GENERAL INFORMATION:
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                 Sequence 473, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: PA104
CURRENT FILING DATE: 2000-03-08
CURRENT FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 473
LENGTHE 259
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149 AspAlaIleGlnGluAlaCysAlaArgAlaGlyGlyArglleAlaValProArgAsnPro 168
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169 GluGluAsnGluAlaIleAlaSerPheValLysLysTyrAsnThrTyrAlaTyrValGly 188
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FRIOR APPLICATION NUMBER: 09/746,491
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 10/055,569
PRIOR FILING DATE: 2001-10-26
NUMBER OF SEQ ID NOS: 169
SOFTWARE: CHRASGGLIST version 0.1
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US-10-336-603A-100
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APPLICANT: Rosen et al.; TILLE OF INVENTION: Nacleic Acids, Proteins and Antibodies; FILE REFERENCE: PA104; CURRENT APPLICATION NUMBER: US/09/925,302; CURRENT FILING DATE: 2001-08-10; PRIOR APPLICATION NUMBER: PCT/US00/05918; PRIOR PILING DATE: 2000-03-08; PRIOR PILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 896; SOFTWARE: Patentin Ver. 2.0; SEQ ID NO 473;
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Matches:
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Mismatches:
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OTHER INFORMATION: Xaa
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LOCATION: (61)
OTHER INFORMATION: X
NAME/KEY: SITE
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; OTHER INFORMATION:
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Best Local Similarity:
Query Match:
DB:
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NAME/KEY: SITE
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TITLE OF INVENTION: Peptides with Antioxidant and Antimicrobial Properties
FILE REFERENCE: 10738-31
CURRENT APPLICATION NUMBER: US/10/312,829
CURRENT FILING DATE: 2003-08-04
PRIOR PELLOATION NUMBER: PCT/US01/2126
PRIOR FILING DATE: 2001-06-29
PRIOR FILING DATE: 2000-06-30
NUMBER OF SEQ ID NOS: 17
SOFFWARE: Patentin version 3.1
SEQ ID NO 10
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16 ProLeuAlaLeu***LeuIleLeuMetAlaAlaSerGlyAlaAlaCysGluValLysAsp
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|GluGlyLysPheThrTyrProThrGlyGluSerLeuValTyrSerAsnTrpAlaProGly 118
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19 LeuGlnAlaAlaPheSerGlnTyrLysLysValGluLeuPheProAsnGlyGlnSerVal
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APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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| AsnAspArgAlaCysGlyGluLysArgLeuValValCysGluPhe 153
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Mismatches:
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                                                                                          Matches:
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Patent No. US20020072067A1
GENERAL INFORMATION:
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Grimaldi, J.Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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Paoni, Nicholas F.
Roy, Margaret Ann
Stewart, Timothy A.
Tumas, Daniel
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Goddard, Audrey
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Botstein, David
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TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                  Percent Similarity:
Best Local Similarity:
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                            US-10-312-829-10
                                                         Alignment Scores
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1998-06-11 NUMBER: 60/088876 1998-06-12 NUMBER: 60/089105 1998-06-12 NUMBER: 60/089440 1998-06-16 NUMBER: 60/089512 1998-06-16 NUMBER: 60/089514 1998-06-17 1998-06-17 1998-06-17 1998-06-17 1998-06-17 1998-06-17	200 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	- 90-
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APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696 APPLICATION NUMBER: 60/090662 APPLICATION NUMBER: 60/090862 APPLICATION NUMBER: 60/090863 FILING DATE: 1998-06-26 APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/091360 APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091474 APPLICATION NUMBER: 60/091544 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091519 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091626 APPLICATION NUMBER: 60/091636 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091638 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091978 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091982 APPLICATION NUMBER: 60/091982 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-07 APPLICATION NUMBER: 60/091982 FILING DATE: 1998-07-09 APPLICATION NUMBER: 60/092182	Alignment Scores:  Pred. No.: 304.50 Matches: 84 Score: 34.73\$ Conservative: 39 Percent Similarity: 30.55\$ Mismatches: 96 Query Match: 22.31\$ Indels: 56 DB: 9	54-536-2 (1-747) x US-09-989-722-357 (1-271)	9 GITTCCATCACTCCTTCTCCTCAGTATGGTGGCAGCGTCTTACTCAGAAACTGT 68 :::   :::	SATIGCCIGIAGCICICCAGGCAT 1	30	N	162 CACCAAGGGAGAAAAGGCGGAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCC 218	219 TGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACC 269	270 AAAGGGCCAAAAAGGAGACCCTGGA294			354 AATGGCACGTATCAAAAAGTGGCTGACCTTCTCTGGGCAAACAAGTTGGGAACAAGTT 413 :::    :::     :::	414 CTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGGGCGTTGTGTGTG	yrAlaAspAlaGl
PRIOR PRIOR	Alignment Pred. No. Score: Percent S Best Loca Query Mat DB:	US-10-054	QY	δλ	g ò	<b>2</b> 40	ζζ G	çy Db	8 6	d &	අු	<b>&amp;</b> 8	ò	ପ୍ର

Search completed: June 18, 2004, 21:13:33 Job time: 54 secs

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                                                                          June 18, 2004, 20:57:11; Search time 21 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd

    protein search, using frame_plus_n2p model

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LNRBPS
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LNRTPS
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Maximum DB seq length: 2000000000
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Match Length DB
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2: pir2:*
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4: pir4:*
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•					pulmonary surfacta	scavenger receptor	collectin liver 1	IGE Fc receptor, 1	hepatic lectin - c	IGE Fc receptor II	complement Clq B c	complement protein	gelatin-binding 28	complement subcomp	collagen alpha 3(I	3	collagen alpha 1(X	albha	alpha	collagen alpha 1(X	complement subcomp	collagen alpha 4(I	tetranectin precur	collagen alpha 1(X	н	complement subcomp	complement supcomp	collagen alpha 3(I	collagen alpha 2(I	complement subcomp	collagen alpha 1(I
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## ALIGNMENTS

mannose-binding lectin precursor [validated] - human

N,Alternate names: mannan-binding protein
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1989 #sequence revision 30-Sep-1991 #text change 08-Dec-2000
C;Accession: JIO115; 805641; Ā34978; JIO027; JX0319; PC2188; A32266
C;Accession: JIO115; 805641; Ā34978; JIO027; JX0319; PC2188; A32266
J, Exp. Med. 170, 1175-1189, Li, Day, L.; Deignan, E.; Bruns, G.; Morton, C.C.; Ezekowitz, R. A;Title: The human mannose-binding protein gene. Exon structure reveals its evolutionary A;Reference number: JL0115; MuID:90010778; PMID:2477486

A; Molecule type: DNA A; Residues: 1-248 <SAS. A; Residues: 1-248 <SAS. A; Cross-references: EMBL:X15422; NID:g34486; PIDN:CAA33462.1; PID:g34487 A; Cross-references: EMBL:X15422; NID:g34486; PIDN:CAA33462.1; PID:g34487 R; Taylor, M.E.; Brickell, P.M.; Craig, R.K.; Summerfield, J.A. B; Taylor, M.E.; Brickell, P.M.; Craig, R.K.; Summerfield, J.A. A; Title: Structure and evolutionary origin of the gene encoding a human serum mannose-b: A; Reference number: S05641; MUID:90073571; PMID:2590164

A;Accession: S05641

A;Molecule type: DNA A;Residues: 1.248 <TAX> A;Cross-references: EMBL:X15954; NID:g34480; PIDN:CAA34079.1; PID:g1212951 A;Accession: A34978

A;Molecule type: protein
A;Residues: 'X',22-24,'X',26,'X',28-31,'X',33-34,'X',36,'XXXX',41-50 <TAY2>
A;Residues: 'X',22-24,'X',26,'X', Herman, G.A.
B;Reckowitz, R.A.B.; Day, L.E.; Herman, G.A.
J. Exp. Med. 167, 1034-1046, 1988
A;Title: A human mannose-binding protein is an acute-phase reactant that shares sequence A;Reference number: JL0027; MUID:88171281; PMID:2450948

A; Accession: JL0027

A;MOlecule type: mRNA A;Residues: 1-2,'C',4,'IT',8,'S',10-57,'R',59-60,'GT',63-106,'PGCLRK',113,'SSANRNGTYQ',: R;Kurata, H.; Sannoh, T.; Kozutsumi, Y.; Yokota, Y.; Kawasaki, T. B:Diochem. 115, 1148-1154, 1994 A;Title: Structure and function of mannan-binding proteins isolated from human liver and A;Reference number: JX0319; MUID:95073978; PMID:7982896

A; Accession: JX0319

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MANDOSE-binding lectin C precursor - mouse

MANDOSE-binding lectin C precursor - mouse

MANDOSE-binding lectin C precursor - mouse

C,5pecies Mas manaculus (Manuse mouse)

C,5pecies Mas manaculus (Manuse mouse)

C,5pecies Mas manaculus (Manuse mouse)

MACCESSION: 18651, 886666, A4554; (A2574

R,5asarry, R.; Ang J. 13-110, 1936

MACCESSION: 18651, 886666, A4554; (A2574

MACCESSION: 18651, 186666, A4554; (A2574

MACCESSION: 18651, 186666, A4554; (A2574

MACCESSION: 18651, 18666, MALDISSIONED MANASOLO, 1, PDD:977288

MACCESSION: 18651, 18666, MALDISSIONED MANASOLO, 1, PDD:977288

MACCESSION: 18651, MALDISSIONED MANASOLO, 1, PDD:977288

MACCESSION: 18666, MALDISSIONED MANASOLO, 1, PDD:977288

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MACCESSION: 18666, MALDISSIONED MALDISSIONED MALDISSIONED MANASOLO MANASOL
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Indels:
Gaps:
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57.88%
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No.:
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                                                                A; Residues: 1-20 <KUR2>
A; Experimental source: liver and serum
C; Comment: Mannose-binding lectins are opsonins that are important in host defense again
C; Comment: This protein is a Ca2+-requring animal lectin specific for mannose and N-acet
C; Genetics:
                                                                                                                                                                                 A/Cross-references: GDB:120167; OMIM:154545

A/Map position: 10q11.2-10q11.2

A/Map position: 10q11.2-10q11.2

A/Map position: 10q11.2-10q11.2

A/Map position: 10q11.2-10q11.2

C/Superfamily: mannose-binding lectin; C-type lectin homology

F/1-20/Domain: signal sequence #status predicted <SIG>
F/1-20/Domain: mannose-binding lectin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                         F;42-99/Region: collagen-like
F;128-244/Domain: C-type lectin homology <LCH>
F;47,73,79,82,88/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
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          A;Residues: 1-248 <KUR1>
A;Accession: PC2188
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Query Match:
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                                                 A: Molecule type: mRNA
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A, Molecule type: mRNA
A, Residues: 86, 'EL', 89-97 < CHI>
B, Wada, M.; Itoh, N.; Ohta, M.; Kawasaki, T.
U. Biochem. 111, 66-73, 1992
J, 1992
A, Pitle: Characterization of rat liver mannan-binding protein gene.
A, Reference number: JX0201, MUID: 92299655; PMID:1607365
A, Rocession: JX0201
A, Molecule type: DNA
A, Residues: 1-244 < WAD>
A, Residues: 101, 135-144, 1987
A, Title: Primary structure of rat liver mannan-binding protein deduced from its cDNA seq A, Reference number: A26798; MUID:87194686; PMID:3032924
A, Reference number: A26798
A, Residues: 1-244 < OKA>
A, Molecule type: MRNA
A, Residues: 1-244 < OKA>
A, Molecule type: MRNA
A, Residues: 1-244 < OKA>
A, Cross-references: GB:X05023; NID:956634; PIDN:CAA28687.1; PID:956635
C, Comment: The molecule contains six identical chains, occurring as disulfide-bonded dim C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannos C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannos C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannos C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannos C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannos C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannos C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannos C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannos C, Comment: Mannan-binding proteins are calcium ion-dependent and are specific for mannan-binding proteins are calcium ion-dependent and are specific for mannan-binding proteins are calcium ion-dependent and are specific for mannan-binding proteins are calcium ion-dependent and are specific for mannan-binding pr
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97 ValGluPheAspThrThrAsnIleAspLeuGluIleAlaAlaLeuArgSerGluLeuArg 116
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117 AlaMetArgLysTrpValLeuLeuSerMetSerGluAsnValGlyLysLysTyrPheMet 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;124-24//Domain: C-type lectin homology <LCH>
F;29,34/Disulfide bonds: interchain #status predicted
F;69/Modified site: 4-hydroxyproline (Pro) #status experimental
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Matches:
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C; Superfamily: mannose-bindir
C; Keywords: calcium; endopla:
F;1-18/Domain: signal sequenc
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A; Reference number: A24791; MUID:86196130; PMID:3009480
A; Accession: A24791
A; Accession: A24791
A; Residues: 1-244 < DRI>
A; Coss. references: GB MUID:01 dding the amino end of the mature protein, was confirm A; Cote: part of the sequence, including the amino end of the mature protein, was confirm R; Childs, R.A.; Feizi, T.; Yuen, C.T.; Drickamer, K.; Quesenberry, M.S.
J. Biol. Chem. 265, 20770-20777, 1990
J. Biol. Chem. 265, 20770-20777, 1990
A; Prittle: Differential recognition of core and terminal portions of oligosaccharide ligan A; Reference number: A38322; MUID:91065871; PMID:2249985
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mannose-binding lectin C precursor - rat
C;Species attus norvegicus (Norway rat)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 22-Jun-1999
C;Accession: A24791; A38322; JX0201; A26798
R;Drickamer, K:, Dordal, M.S.; Reynolds, L.
K;Drickamer, K:, Dordal, N.S.; Reynolds, L.
J. Biol. Chem. 261, 6878-6887; 1986
A;Title: Mannose-binding proteins isolated from rat liver contain carbohydrate-recogniti
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|MetSerllePheThrSer-----PheLeuLeuCysValValThrValValTyrAla
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                       ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCTGAGTATGGTGGCAGCGTCTTACTCA
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homohexamer; hydroxyproline

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244 151 34 34 57

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240

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pulmonary surfactant protein D precursor - human
NiAlternate names: SP-D
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (masternation of human surfactant protein D (SP-D)
S;Crouch, E.; Rust, K.; Veile, R.; Donis-Keller, H.; Grosso, L.
A;Title: Genomic organization of human surfactant protein D (SP-D). SP-D is encoded on C
A;Reference number: A45225; MUID:93155122; PMID:8428971
A;Residues: 1-375 < CRO
A;Residues: 1-375 < CRO
A;Residues: GB:L05483; GB:L05484; GB:L05485; NID:g292505; PIDN:AABS9450.1; PID:g
A;Residues: Genomic organization and cDNA cloning of human lung surfactant protein A;Reference number: S23434; MUID:92322003; PMID:133284
A;Residues: 1-30."T", 32-121,"P', 123-179,"A', 181-375 < LUJ1>
A;Residues: LyDe: mRNA
A;Residues: LyDe: mRNA
A;Residues: LyDe: mRNA
A;Residues: LyDe: mRNA
A;Residues: LyDe: MSA
A;Res
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A; Residues: 202-257 <HOP>
R; Rust, K; Grosso, L; Zhang, V; Chang, D; Persson, A; Longmore, W; Cai, G.Z.; Crou
Arch. Biochem. Biochem. Biophys. 290, 116-126, 1991
A; Title: Human surfactant protein D: SP-D contains a C-type lectin carbohydrate recognit
A; Reference number: S18382; MUID:91378578; PMID:1898081
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A; Residues: 'F', 60-205,'P', 207-374,'HF' < RUS>
A; Residues: 'F', 60-205,'P', 207-374,'HF' < RUS>
A; Cross-references: GB=L054865; NID:q292505
A; Note: corrections to this sequence are reported in reference A56776
B; Crouch, E.; Persson, A.; Chang, D.
Am. J. Pathol. 142, 241-248, 1993
A; Title: Accumulation of surfactant protein D in human pulmonary alveolar proteinosis.
A; Reference number: A56776; MUID:93142849; PMID:8424457
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| 154 ||ProArgAsnAlaGluGluAsnLysAlaIleGlnGluValAlaIaysThrSerAlaPhe
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A,Molcoule type: protein
A;Residues: 214-234, X',236,'XX',239-241 <LUU2>
R;Hoppe, H.J.; Barlow, P.N.; Reid, K.B.M.
ERES Lett. 344, 191-195, 1994
A;Title: A parallel three stranded alpha-helical bundle at
A;Reference number: S44420; MUID:94244769; PMID:8187882
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A,Residues: 1-238 cDR1-

R,Drickamer, K., McCreary, V.
J. Biol. Chem. 262, 2582-2589, 1987

A,Title: Exon structure of a mannose-binding protein gene reflects its evolutionary rela
A,Recession: A29556
A,Rocession: A29556; MUID:87137502; PMID:3029088
A,Rocession: A29556; MUID:87137502; PMID:3029088
A,Rocession: A29556
A,Residues: 1-155, K.,157-238 cDR2-
A,Residues: L-155, K.,157-238 cDR2-
A,Residues: L-155, K.,157-238 cDR2-
A,Residues: L-155, K., 157-2454, 1987
A,Residues: L-155, K., 157-454, 1987
A,Rice a, K.; Sannoh, T.; Rawasaki, N.; Rawasaki, T.; Yamashina, I.
R; Reda, K.; Sannoh, T.; Rawasaki, N.; Rawasaki, T.; Yamashina, I.
A,Rocession: A27799; MUID:87222358; PMID:3584121
A,Recenter number: A27799; MUID:8722358; PMID:3584121
A,Rece
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                                                                                                                                                                         A;Cross references: GDB:132674; OMIN:178635
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
C;Reywords: blocked amino end; calcium; glycoprotein; hydroxylysine; hydroxyproline; lun
F;1-20/Domain: signal sequence #status predicted <SIG>F;1-375/Porduct: pulmonary surfactant protein D #status predicted <NG>F;21-45/Domain: non-collagenous #status predicted <COb-F;23-375/Domain: non-collagenous #status predicted <COb-F;23-375/Domain: collagenous #status predicted <COb-F;23-375/Domain: C-type lectin homology <LCH>F;254-373/Domain: C-type lectin homology <LCH>F;281-373/Domain: G-type lectin homology <LCH>F;281-373/Jomain: G-type lectin homology school #status predicted
F;281-373,351-365/Disulfide bonds: #status predicted
A Residues: 46-58, FF, 60-62, E, 64-72; 223-227, XY, 229-239, PY, 241-245, XY, 247-256, XY, 25 A; Cross-references: PIDN:AAB25037.1; PID:g263973; PIDN:AAB25038.1; PID:g263974 A; Experimental source: bronchoalveolar lavage A; Note: sequence extracted from NCBI backbone (NCBIP:123024, NCBIP:123023); sequence mod C; Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t C; Comment: This protein is synthesized by alveolar type II cells.
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AlaProGlyMetGlnGlySerAlaGlyAlaArgGlyLeuAlaGlyProLysGlyGluArg 168
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|GlyValProGlyGluArgGlyValProGlyAsnThrGlyAlaAlaGlySerAlaGlyAla 188
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A, Keterence number: JC2396
A, Recestion: JC2396
A, Recestion: JC2396
A, Recestion: JC2396
A, Recestion: JC236
A, Recestion: JC236
A, Recestion: JC22, 157-162, 1993
B, Libia.
B, Residues: L127, HV, 174-217, AV, 219-271, VV, 273-371
C, LUJD
A, Accession: S, Libia.
B, Libia.
A, Residues: L123, HV, 174-217, AV, 219-271, VV, 273-371
C, LUJD
A, Recentered and Ber: RELEXATION A, RID:9395267, PIDN:CAS5065.1; PIDN:GAS5065.1; PIDN:G
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R;Malhotra, R.; Laursen, S.B.; Willis, A.C.; Sim, R.B.
Biochem. J. 237, 15-19, 1993
A;Title: Research Communication. Localization of the receptor-binding site in the colle
A;Reference number: S34054; MUID:93319501; PMID:8328957
                                                                                                                                                                                                                                                                                                                                                                                                                                              NyAlternate names: C3b-binding protein
NyContains: conglutinin-N
C.Species: Bos primigenius taurus (cattle)
C.Species: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 16-Jun-2000
C.Soccession: JN0450; JC2396; S3235; A2340; S35679; S35644; I46010; A29416; S34054
R;Suzuki, Y.; Yin, Y.P.; Makino, M.; Kurimura, T.; Wakamiya, N.
Biochem: Biophys. Res. Commun. 191, 335-342, 1993
A;Title: Cloning and sequencing of a cDNA coding for bovine conglutinin.
A;Reference number: JN0450; MUID:93213261; PMID:8460993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conglutinin: A C-type
A Molecule type: mRNA
A Residues: 1-371 CSUZ>
A Residues: 1-371 CSUZ>
A CROSS-references: DDBJ:D14085; NID:g285643; PIDN:BAA03170.1; PID:g285644
A Experimental source: liver
R Kawasaki, N.; Itoh, N.; Kawasaki, T.
B iochem: Biophys: Res. Commun. 198, 597-604, 1994
A Title: Gene organization and S. flanking region sequence of conglutinin: A Reference number: JC2396; MUID:94128104; PMID:8297370
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D. cDNA and deduced
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surfactant protein D - rat
C;Species: A42046
C;Species: A42046
C;Accession: A42046
R;Shimizu, H.; Fisher, J.H.; Papst, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelke
R;Shimizu, H.; Fisher, J.H.; Papst, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelke
R;Shimizu, H.; Fisher, J.H.; Papst, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelke
R;Shimizu, H.; Fisher, J.H.; Papst, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelke
R;Shimizu, H.; Fisher, J.H.; Papst, P.; Benson, B.; Lau, K.; Mason, R.J.; Voelke
R;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1.374 cSHI>
A;Residues: 1.374 cSHI>
A;Cross-references: GB:MB1231; NID:g207035; PIDN:AAA42170.1; PID:g207036
A;Experimental source: lung
A;Note: sequence extracted from NCBI backbone (NCBIN:76027, NCBIP:76031)
C;Superfamily: pulmonary surfactant protein D; C-type lectin homology
F;253-372/Domain: C-type lectin homology cLCH>
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64 AspProGlyLeuProGlyProMetGlyLeuSerGlyLeuProGlyProArgGlyProVal
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                      TCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCC
                                                                                              GGAAATAGACTGACCTACACAAAACTGGAACGAGGTGAACCCAACAATGCT-----GGT
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1110
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128
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Matches:
Conservative:
Mismatches:
Indels:
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LysGlnLeuLeuVallleCysGluPhe 371
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Pred. No.:
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C; Superfamily: pulmonary surfactant protein D; C-type lectin homology
C; Superfamily: pulmonary surfactant protein D; C-type lectin homology
C; Seywords: calcium binding; 4; Yroporotein; hydroxylyaine; hydroxyproline
F; 1-20/Domain: signal sequence #status predicted <SIG>
F; 1-21/Product: conglutinin #status predicted <MAT>
F; 46-214/Region: collagen-like
F; 5-371/Product: conglutinin-M #status predicted <MAZ>
F; 248-369/Domain: C-type lectin homology &LCH>
F; 248-369/Domain: C-type lectin homology &LCH>
F; 387,99,135,141,159,162,198,210/Modified site: 5-hydroxylysine (Lys) #status experime
F; 78,96,108,111,129,132,147,153,171,195/Modified site: 4-hydroxyproline (Pro) #status experime R; 337/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                    A;Cross-references: EMBL:U06860; NID:g507183; PIDN:AAB60624.1; PID:g514256
C;Comment: This protein mediates the agglutination of erythrocytes with antibody and com
C;Comment: This protein is a Ca2+-dependent serum lectin specific for N-acetylglucosamin
C;Genetics:
                          T.B.; Tauber, A.I.; Sastry
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    486
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LysasnAlaTyrLeuSerMetAsnAspIleSerThrGluGlyArgPheThrTyrProThr 322
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91
39
74
25
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-371 <LIO>
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441.50
56.77*
39.74*
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S.B.; Jensenius, J.C.; Holmsko
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PMID:8486682
                                                                                                                                                                                                                                               ---TCAGAAAGAAAGCTCTGCAAACAGAAATGGCACGTATC 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 GlnProGluAsnCysValGluIlePheProAspGlyLysTrpAsnAspValProCysSer 362
                                                                                                                                                                                                                                                                                                                                                                                                  NyAlternate names: lectin CL-43

NyAlternate names: lectin CL-43

C.Species: Bos primigenius taurus (cattle)

C.Species: Bos primigenius taurus (cattle)

C.Accession: A55570; A46689

R.Lim, B.L.; Willis, A.C.; Reid, K.B.M.; Lu, J.; Laursen, S.B.; Jensenius, J. Biol. Chem. 269, 11820; 1184, 1994

A;Title: Primary structure of bovine collectin-43 (CL-43). Comparison with c A;Reference number: A53570; MUID:94216283; PMID:8163480

A;Status: preliminary
118 TCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAG
                     -GGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAG
                                                                                                                                                                                                                                                                                                                                     GlnArgValThrIleLeuAspGlyHisLeuArgArgPheGlnAsnAlaPheSerGlnTyr
                                                                                                       163 GlyAlaProGlyGluThrGlyAlaProGlyHisAlaGlyValThrGlyProSerGlyAla
                                                                                                                                                                       TTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::: |||:::||| ::: ||| 303 LysasnalaTyrLeuSerMetAsnaspIleSerThrGluGlyArgPheThrTyrProThr
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A,Residues: 1-301 <LIM>
A);Cross-references: GB:X75912
R;Holmskov, U.; Teisner, B.; Willis, A.C.; Reid, K.B.; Jensenius, J.C.
U. Blod. Chem. 268, 10120-10125, 1993
A;Title: Purification and characterization of a bovine serum lectin (C
A;Reference number: A46689; MUID:93252891; PMID:8486682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: serum
A;Note: sequence extracted from NCBI backbone (NCBIP:131234)
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                                                                          GGGGAACCAGGCCAA--
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Cibate: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Aug-1999
Cipacession: 145878
Ribiou, L.S.; Sastry,
Ribiou, L.S.; Sastry
Gene 141, 277-281, 1994
A.Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization capter number: 145878
A.Title: Bovine conglutinin (BC) mRNA expressed in liver: cloning and characterization capter number: 145878
A.Accession: 145878
A.Accession: 145878
A.Accession: 145878
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Accession: 1371 cllo
A.Residues: 1-371 cllo
A.Residues: 1-371 cllo
A.Residues: 1-371 cllo
A.Coss-references: GB:L18871; NID:9495012; PIDN:AAA20126.1; PID:9495013
C.Superfamily: pulmonary surfactant protein D; C-type lectin homology
F;248-369/Domain: C-type lectin homology clCH>
               309
                                            LysGlyGluArgGlyAlaProGlyGluGlnGlyAlaProGlyAsnAlaGlyAlaAlaGly 183
                                                                                                                     ProAlaGlyProAlaGlyProGlnGlyAlaProGlySerArgGlyProProGlyLeuLys 203
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224 AlaAlaLeuArgGlnGlnMetGluAlaLeuAsnGlyLysLeuGlnArgLeuGluAlaAla 243
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                                                                                                                                                                                               GlyAspArgGlyAlaProGlyAspArgGlyIleLysGlyGluSerGlyLeuProAspSer
                                                                                                                                                                                                                                  AGCCTGGCTGCCTCAGAAAGCTCTGCAAACAAAGAAATGGCAGGTATC-----
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Mismatches:
Indels:
Gaps:
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| SerGlyArgGlnGlySerMetGlyProProGlyThrProGlyProLysGlyGluProGly
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protein D; C-type lectin homology
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Matches:
Conservative:
Mismatches:
Indels:
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 C;Superramııy. r...
C;Keywords: lectin
F;177-299/Domain: C-type lectin homology
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                                                       3.36e-29
418.00
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30.62%
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193 GGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCT 44 AspGlyArgAspGlyValLysGlyAspProGlyProProGlyProMetGlyProProGly 148 GATGGGCGTGATGGCACCAAGGGAAAAAGGGGGAACCAGGCCAA-----

313 AGTAGCCTGGCTGCCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCACGTATCAAAAAG 372

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-----LeuProAlaTyrLeuAspGluGluLeuGlnAlaThrLeuHisGluLeuArgHis

AAGACCTGCCCTGCAGTGATTGCCTGTAGCTCTCCAGGCATCAACGGCTTCCCAGGCAAA 147

CITCTCCTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTGACCTGTGAGGATGCCCAA

(1-247)

x LNRBPS

US-10-054-536-2 (1-747)

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Percent Similarity: Best Local Similarity:

Query Match:

26 IleGlySerProGlyIle-----ProGlyThrProGlySerHisGlyLeuProGlyArg

43

HisAlaLeuGlnSerIleGlyValLeuSerLeuGlnGlySerMetLysAlaValGlyGlu 135

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TGGCTGACCTTCTCTGGGC--------

------AAACAAGTTGGGAAC 408

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A,Accession: A2991
A,Molecule type: MRNA
A,Residues: 1-247 eNGS
A,Coss-references: GB:.03542; NID:g165705; PIDN:AAA31465.1; PID:g165706
A,Coss-references: GB:.03542; NID:g165705; PIDN:AAA31465.1; PID:g165706
A,Note: 12-Pro was also found
A,Note: the amino end of the mature protein is blocked
C,Comment: Pulmonary surfactant is a complex of phospholipids and proteins that lowers t
C,Comment: This protein is a sianglay/coprotein synthesized by alveolar type II cells. It
C,Comment: This protein is a sianglay/coprotein synthesized by alveolar type II cells. It
C,Comment: This protein is a sianglay. C-type lectin homology
C,Superfamily: mannose-binding lectin; C-type lectin homology
C,Superfamily: mannose-binding lectin; C-type lectin homology
C,Superfamily: asserved anino end; alveolar proteinosis; calcium; gaseous exchange; glyco
F;1-15/Domain: signal sequence #status predicted <SIG.
F;1-247/Product: pulmonary surfactant protein A #status predicted <MAT>
F;27-99/Region: collagen-like
F;126-245/Domain: C-type lectin homology <LCH>
F;16-245/Domain: c-type lectin homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sed
                                                                                                                                                                                                                                                                                pulmonary surfactant protein A precursor - rabbit
N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated
C;Species: 07roColagus cuniculus (domestic rabbit)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 16-Jul-1999
C;Accession: A29931
K;Boggaram, V; Qing, K; Mendelson, C.R.
J. Biol. Chem. 263, 2939-2947, 1988
A;Pitle: The major apoprotein of rabbit pulmonary surfactant. Elucidation of primary seq
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AGTTCTTCCTGACCAATGGTGAAATAATGACCTTTGAAA	100 GlyAspThrGlyProProGlyProProGlyProAlaGlyArgGluGlyPro 119     220
4.69e-29 Length: 369 416.50 Matches: 108 Astrict: 39.46\$ Mismatches: 108 Astrict: 29.19\$ Mismatches: 39 Indels: 125 Gaps: 125 Gaps: 106  (1-747) x \$33603 (1-369)  Trictrorrocarcacarcacarcacacacacacacacacacaca	Oy 589 GATCTGACAGGAATAGACTGACCTACACAAACTGGAACGACGACACACAC

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A,Accession: B25720
A,Molecule type: mRNA
A,Residues: 1-248 <PLO>
A,Cross-references: GB:R03475
A,Note: part of the sequence was confirmed by protein sequencing
A,Note: part of the sequence was confirmed by protein sequencing
A,Note: clones corresponding to two different proteins were sequenced. Corranslational m A,Note: clones corresponding to two different proteins were sequenced. Cotranslational m G,Genetics:
A,Genetics:
A,Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pulmonary surfactant protein A precursor (clone 1A) - human N;Alternate names: pulmonary surfactant 32K apoprotein; pulmonary surfactant-associated C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 31-Dec-1990 #text_change 16-Jul-1999 C;Accession: B25720 R;Ploros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.; A;Ploros, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.; A;Flores and characterization of cDNA clones for the 35-kDa pulmonary surfacta A;Feference number: A25720; MUID:86250832; PMID:3755136
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                                                                                                                                                                                                                                                                                                            CCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTGACCTGTGAGGAT
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                                                                                                                                                                                             ||||||| ||||||| :::::: |||:::
169 GluGluAsnGluAlaIleAlaSerIleAlaLysLysTyrAsnAsnTyrValTyrLeuGly
                                                                                                                                                      ATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCTAC
                                                                                                                                                                                                                                                                                                                                                                                        CTGAAAAATGGCCAGTGGAATGACGTCCCTGCTCCACCTCCCATCTGGCCGTCTGAG
                                       GAAGCCTTCCTGGGC
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Mismatches:
Indels:
                                       505 GCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG-
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A; Reference number: JS0034; MJID:89000785; PMID:2901856
A; Contents: 1.6 kb cDNA
A; Accession: JS0034
A; Accession: JS0034
A; Molecule type: mRNA
A; Residues: 1-248
A; Molecule type: mRNA
A; Residues: 1-248
A; Accession: JS0034
A; Residues: 1-248
A; Residues: 1-248
A; Accession: S23183; MUID:92298987; PMID:1606951
A; Title: Characterization of the rat pulmonary surfactant protein A promoter.
A; Reference number: S23183; MUID:92298987; PMID:1606951
A; Accession: S23183
A; Molecule type: DNA
A; Residues: 1-32
A; Accession: S23183
A; Molecule type: DNA
A; Residues: 1-32
A; Accession: S23183
A; Molecule type: DNA
A; Residues: 1-32
C; Comment: This protein is a sialogly coprotein synthesized by alveolar type II cells. It pendent on the presence of calculm ions.
C; Comment: This protein is a sialogly coprotein synthesized by alveolar type II cells. It pendent on the presence of calculm ions.
C; Comment: Size heterogeneity of these proteins arises from posttranslational modificati C; Superfamily: mannose-binding lectin, c-type lectin, homology
C; Keywords: alveolar proteinosis; calculm; gaseous exchange; glycoprotein; hydroxyprolin F;1-20/Domain: signal sequence #status predicted <SIG>F;21-248/Product: pulmonary surfactant protein A #status experimental <AMAT>F;12-246/Domain: calbagen-like
F;17-246/Domain: carbohydrate (Asm) (covalent) #status absent
F;207/Binding site: carbohydrate (Asm) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ThrdluLeuTyrGluileLysHisGlnIleLeuGlnThrMetGlyValLeuSerLeuGln 128
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us-10-054-536-2.rpr

ò	202 GGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGG 249	F;30,33,36,42,54,57,63,76,79,82,91,97/Modified site: 4-hydroxyproline (Pro) #status pre F;207/Binding site: carbohydrate (Asn) (covalent) #status predicted
qu	60MetGlyProProGlyGluThrProCysProProGlyAsnAsnGlyLeuProGly 77	Scores:
δ	GCCAAAAGGAGACCCTGGAA	5.09e-27 Length: 393.50 Matches:
qa	78 AlaProGlyValProGlyGluArgGlyGluLysGlyGluProGlyGluArgGlyFroPro 97	Percent Similarity: 50.57% Conservative: 36 Best Local Similarity: 36.78% Mismatches: 90
ò	307 GGTGALAGTAGTGCTGGCTGCCTCAGAAAGAAAA 339	Indels: Gaps:
QQ	98 GlyLeuProAlaHisLeuAspGluGluLeuGlnAlaThrLeuHisAspPheArgHisGln 117	US-10-054-536-2 (1-747) x LNHUP6 (1-248)
کن بری	CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAA 3	22 CCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTGACCTGTGAGGAT
1 8	TOURS THE ROLL TOURS TO BE A STATE OF THE PROPERTY OF THE PROP	5 FIOLEUALALEUASDLEUILELEUMETALAALASETGIYALAALACYSGLUVAILYSASD
g qq	dlySerIleMetThrValGlyGluLysValPheSerSerAsnGlyGlnSerIleThrPhe 1	by scucramakancriccincarianingcrigiagcraftcangeartrancearrac
λŏ	445 GAAAAAGTGAAGGCCTTGTGTGTGAAGTTCCAGGCCTCTGTGGCCACCCCCAGGATGCT 504	Qy 142 GGCAAAGATGGGGGTGATGGCACCAAGGGAAAAAAGGGGGAACCAGGCCAAGGGTCAGA 201
qa	149 AppalaileGinGlualaCysAlaArgAlaGlyGlyArgileAlaValProArgAsnPro 168	:::
Qy qq	505 GCAGAGAATGGAGCCATTCAGAATCTCATCAAGAGGAAGCCTTCCTGGGC 555  169 Gluglukanginalaflaalasephadalidefuserunaammenen jameusisti 100	202 GGCTTACAGGCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGG
ò		buMerGiykrokrokiydiuMetkrokyskrokrokiyAsnAspGiyLeuProGiy
qq		VY 250 CUITLIGGGITACCAAGAGGGCCAAGAGGGCCCTGGAAAAAGTCCGGAT 306  DD 78 AlaProdly11e
λö	616 ACAAACTGGAACGAGGGGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGCTA 675	GGTGATAGCCTGGCTGCCTCAGAAAGAAA
qa		98 GlyLeuProAlaHisLeuAspGluGluLeuGlnAlaThrLeuHisAspPheArgHisGln
ζŎ	676 CIGAAAAAIGGCCAGIGGAAIGACGICCCCTGCTCCCCATCTGGCCGTCTGTGAG 735	Qy 340 GCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCTCTGGGGAAACAA 399
QQ	228 TyrThrAspGlyGlnTrpAsnAspArgAsnCysLeuTyrSerArgLeuThrlleCysGlu 247	
δ	736 TTC 738	Qy 400
qa	248 Phe 248	Db 129 GlySerIleMetThrValGlyGluLysValPheSerSerAsnGlyGlnSerIleThrPhe 148
RESULT 1	15	Qy 445 GAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCCCCAAGGAATGCT 504
pulmonary N, Alterna	7. to to the true	:::
C;Specie C;Date:	Jul-1999	QY 505 GCAGAGAAIGGAGCCAITCAGAAICTCATCAAGGAGGAAGCCITCCIGGGC 555
C, Acces: R, Floros	sion: A25720 8, J.; Steinbrink, R.; Jacobs, K.; Phelps, D.; Kriz, R.; Recny, M.; Sultzman, L.;	Db 169 GluGluAsnGluAlaileAlaSerPheValLySLySTyrAsnThrTyrAlaTyrValGly 188
J. Biol. A;Title:	tDa pulmon	
A; Relett A; Access	ence number: Az5/20; MULD:86250832; PMLD:3755136 sion: A25720: A25720; MULD:86250832; PMLD:3755136	<pre>Db 189 LeuThrGluGlyProSerProGlyAspPheArgTyrSerAspGlyThrProValAsnTyr 208</pre>
A; Molect A; Residt	11e Type: mkNA 168: 1-248 KFLO> Theforence: MD: MTD: 1005C, WTD: 1005CO, NTD: 1005C	616 ACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGCTA
A; Note:	190670	209 ThrAsnTrpTyrArgGlyGluProAlaGlyArgGlyLysGluGlnCysValGluMet
A;Note: C:Geneti	clones corresponding to two different proteins were sequenced. Cotranslational m	676 CTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCCCATCTGGCCGTCTGGCAG
A;Gene: A;Cross-	GDB:SFTPA1; SF-A; SP-A1 references: GDB:119593; OMIM:178630	DD 228 TyrThrAspGLyGlnTrpAsnAspArgAsnCysLeuTyrSerArgLeuThrIleCysGlu 247
A; Map pc C; Superf	-	248 Phe
F;1-20/E F;21-248	Fil-20/Domain: signal sequence #status proteincus; calcium; gaseous exchange; glyco Fil-20/Domain: signal sequence #status predicted <sig> Fig. 48/Product: pulmonary surfactant protein A #status predicted <mat></mat></sig>	Search completed: June 18, 2004, 21:03:40
F;127-24 F;21/Moc	46, Domain: C-type lectin homology <lch> lified site: acetylated amino end (Glu) (in mature form) #status predicted</lch>	Job time : 26 secs

us-10-054-536-2.rni

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Sequence 1, Appli
Sequence 25, Appl
Sequence 24, Appl
Sequence 3, Appli
Sequence 1, Appli
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Sequence 24, Appli
Sequence 7, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
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'Ggn2_6/ptodata/2/ina/5A_COMB.seq:*
'Ggn2_6/ptodata/2/ina/5B_COMB.seq:*
'Ggn2_6/ptodata/2/ina/6A_COMB.seq:*
'Ggn2_6/ptodata/2/ina/6B_COMB.seq:*
'Ggn2_6/ptodata/2/ina/PGTUS_COMB.seq:*
'Ggn2_6/ptodata/2/ina/PGTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-198-603C-25
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US-08-355-103B-5
US-09-535-521-26
US-09-535-521-7
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Listing first 45 summaries
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Sequence 3, Appli Sequence 10, Appli Sequence 10, Appli Sequence 9, Appli Sequence 9, Appli Sequence 5, Appli Sequence 5, Appli Sequence 10, Appl Sequence 101, App Sequence 1138, App Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl		PROTEIN IN METHYLOTROPHIC	Length 900; Indels 0; Gaps 0;	GGTGGCAGCGTCTTACTCA 60 	AGTGATTGCCTGTAGCTCT 120 	CACCAAGGGAGAAAAGGGG 180 	AAAGTTGGGGCCTCCAGGA 240 
US-09-776-976-3 US-09-909-57-3 US-09-620-312D-110 US-08-46-911-6 US-09-686-818B-9 US-09-686-818B-9 US-09-776-976-5 US-09-552-204A-10 US-09-552-204A-10 US-09-552-204A-10 US-09-552-204A-10 US-09-512D-1061 US-09-513-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138 US-09-614-124B-1138	ALIGNMENTS	MANNOSE-BINDING 98,603C	Score 747; DB 4; Pred. No. 4.1e-228; 0; Mismatches 0;	ATGICCCTGITICCAICACTCCCTCTCCTTCTCCTGAGIAIGGTGGCAGCGICTTACTCA	GAAACTGTGACTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 	CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAACGGG 	GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCCAGGA 
11276 4 11276 4 12376 4 14517 3 1313 2 1313 2 1313 2 1313 2 1313 2 1313 2 1319 4 1511 4 1729 4 1729 4 1729 4		on US/091981 aymond E. ONE, G. Thor hawn, S. Michael T. EXPRESSION YEARS 90 1098-11-2. 198-11-2.	100.0%; 100.0%; ative	TTCCATCA          TTCCATCA	CCTGTGAG           CCTGTGAG	ACGGCTTC             ACGGCTTC	AAGGGCTC
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R R R R R R R R R R R R R R R R R R R		SULT 1 -09-198-603C-1 Sequence 1, Applicat: Patent No. 6337193 GENERAL INFORMATION: APPLICANT: TULLY, APPLICANT: TULLY, APPLICANT: CALTAGII APPLICANT: ROWING, TITLE OF INVERTION: TITLE OF INVERTION: FILE REFERENCE: A7; CURRENT FILING DATE NUMBER OF SEQ ID NO; SOFTWREY FILING DATE NUMBER OF SEQ ID NO; STEPTENENCE: PATENTING STEPTENENCE: PATENTING TYPE: DNO 1 LENGTH: 900 TYPE: DNO 1 LENGTH: 900 TYPE: DNA ORGANISM: Human ORGANISM: Human	Query Match Best Local Si Matches 747;	1 8	61 6	121 0	181 G
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APPLICANT: TULLY Raymond B. APPLICANT: TULLY Raymond B. APPLICANT: MOYER, SIAWI S. Thomas APPLICANT: MOYER, SIAWI S. TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC TITLE OF INVENTION: YEAST FILLE REFERENCE: A7290 CURRENT APPLICATION NUMBER: US/09/198,603C CURRENT APPLICATION NUMBER: US/09/198,603C CURRENT FILING DATE: 1998-11-24 NUMBER OF SEQ ID NOS: 26 SOFTWARE: SEQ ID NOS: 26 SOFTWARE: SEQ ID NO 26 LENGTH: 714
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                                     TACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTG
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Pred. No. 3.8e-30;
0; Mismatches 290; Indels
                                                                                                                                                                                                                                              ; Sequence 26, Application US/09198603C; Patent No. 6337193; GENERAL INFORMATION:
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Best Local Similarity 53.0%;
Matches 351; Conservative C
                                                                                                             734 AGIICCCIAICIGA 747
                                                                                                                                           AATTCTCTGACTGA 949
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                                                                                                                                                                                                          RESULT 3
US-09-198-603C-26
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Patent No. 6337193
GENERAL INFORMATION:
APPLICANT: TULLY, Raymond E.
APPLICANT: TULLY, Raymond E.
APPLICANT: TULLY, Raymond E.
APPLICANT: SARWN S.
APPLICANT: RONNING, Michael T.
TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC FILE REFERENCE: A7290
CURRENT APPLICATION NUMBER: US/09/198,603C
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
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                 606 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAAGGCAGATTGTGGGATCTGACAGGA
                                                                                                                                                                                                                                                                                                                                                                                                 726 GATIGIGIATIGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT
                                                                                                                                               TCTGTGGCCACCCCCAGGAATGCTGCAGAATGGAGCCATTCAGAATCTCATCAAGGAG
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Pred. No. 5.1e-55;
); Mismatches 106;
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ORGANISM: Mouse
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Best Local Simi
Matches 268;
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Lynch, Richard G
APPLICANT: Yodoi, Jungi
TITLE OF INVENTION: DRA Sequences for Soluble Froms of C
TITLE OF INVENTION: DRA Sequences for Soluble Froms of C
TITLE OF INVENTION: And Methods of Use for Same
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: Bos Moines

CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.0%; Score 67.6; DB 1; Length 8 ilarity 55.6%; Pred. No. 1.8e-11; Conservative 0; Mismatches 104; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
AUPLICATION DATE: US/08/365,103B
FILING DATE: 28-DEC-1994
FILING DATE: 28-usc. CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf N5-24
TELECOMMUNICATION INFORMATION:
TELEFAX: (515) 288-3667
TELEFAX: (515) 288-367
INFORMATION FOR EQI DNO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 885 base pairs
FYPE: nucleic acid
STRANDEDNESS: single
"nbology: linear
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States
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Matches 130; Conserv
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HYPOTHETICAL:
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LOCATION:
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US-09-198-603C-24
Sequence 24, Application US/09198603C
Patent No. 6337193
GENERAL INFORMATION:
APPLICANT: TULLY, Raymond E.
APPLICANT: CALTAGIRONE, G. Thomas
APPLICANT: MOYER, Shawn S.
APPLICANT: MOYER, Shawn S.
TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC
TITLE OF INVENTION: YEAST
FILE REFERENCE: A7290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1173 CAGGTCAAGGGCTCAGGGGCTTGCAGGGCCCTCCAGGGAAACTGGGGGCCTCCAGGAAGTG 1232
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                                                    634 GACTGTGCGGTGATAGAAGACTCTGGAAAATGGAATGATTTAGACTGTTCAAATTCAAAT 693
                    601 AATAGACTGACCTACAAACTGGAACGAGGTGAACCCAACAATGCTGGTTCTGATGAA 660
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                                                                                                        661 GATTGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT
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Pred. No. 3.5e-13;
0; Mismatches 26; Indels 0
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Patent No. 5766943
GENERAL INFORMATION:
APPLICANT: Lynch, Richard G
APPLICANT: Yodoi, Unugi
TITLE OF INVENTION: DAM Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Zarley, McKee, Thomte, Voorhees & Sease 801 Grand Ave. Suite 3200
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COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/198,603C
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 24
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COUNTRY: United States
ZIP: 50309
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Best Local Similarity
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CITY: Des Moines
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US-08-365-103B-3
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Query Match
9.0%; Score 67.6; DB 1; Length 1
Best Local Similarity 55.6%; Pred. No. 1.9e-11;
Matches 130; Conservative 0; Mismatches 104; Indels
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8.4*; Score 62.8; DB 4;
Best Local Similarity 57.7*; Pred. No. 3.7e-10;
Matches 112; Conservative 0; Mismatches 82;
                        TELEFAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                  LENGTH: 1005 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-535-521-24
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ANTI-SENSE: NC
FEATURE:
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; LOCATION:
US-08-365-103B-1
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NAME/KEY: CDS
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Ratent No. 5766943
GENERAL INFORMATION.
APPLICANT: Lynch, Richard G
APPLICANT: Nunez, Raphael D.
APPLICANT: Nunez, Raphael D.
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CLUARESSE: Carley, McKee, Thomte, Voorhees & Sease STREET: 801 Grand Ave. Suite 3200

STATE: lowa Country: United States

ZIP: 50309
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 28-DEC 1994
ATTORNEY/AGENT INPORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: 0irf N5-24
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf N5-24
TELECOMMUNICATION INPORMATION:
TELEPHONE: (515) 288-3667
TELEFRAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 924 base pairs
TYPE: nucleic acid
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LOCATION:
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US-08-365-103B-5
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Patent No. 6410714

GENERAL INFORMATION

APPLICANT: Weber, Eric R.

APPLICANT: Wccall, Catherine A.

ITILE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)

ITILE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

FILE REFERENCE: AL-5

CURRENT APPLICATION NUMBER: 05/09/535,521

CURRENT FILING DATE: 2000-03-24

EARLIER APPLICATION NUMBER: 60/125,913

BARLIER APPLICATION NUMBER: 60/125,913

SANTHARE: PATENTING DATE: 2000-03-24

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTIN Ver. 2.1
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; LOCATION: (1)..(384)
US-09-535-521-7
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US-09-535-521-9/c
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Sequence 7, Application US/0953521

Patent No. 6410714

GENERAL INFORMATION:

APPLICANT: Weber, Eric R.

APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 1GE RECEPTOR (CANINE CD23)

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF

FILE REPERENCE: AL.5

CURRENT APPLICATION NUMBER: US/09/535,521

CURRENT FILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 7

LENGTH: 384
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APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: NOVEL CAUINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: NOVEL CAUINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: NOVEL CAUINE LOW AFFINITY IGE AND USES THEREOF
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: 60/125,913
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER PILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTION OF S. 21
SEQ ID NO 26
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Pred. No. 3.7e-10;
0; Mismatches 82;
                                                                                                                                                                                                            Sequence 26, Application US/09535521 Patent No. 6410714
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Best Local Similarity 57.7%;
Matches 112; Conservative
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ORGANISM: Canis familiaris
FEATURE:
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US-09-535-521-7
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APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 1GE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 1GE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ 1D NOS: 26
SOFTWARE: PATCHIN VET. 2.1
SEQ 1D NO 9
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Pred. No. 3.8e-10;
0; Mismatches 82;
Score 62.8; DB 4;
Pred. No. 3.8e-10;
0; Mismatches 82
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US-09-535-521-10
; Sequence 10, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
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ilarity 57.7%;
Conservative (
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Best Local Similarity 57.7%;
Matches 112; Conservative
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US-09-535-521-9
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169 TATCTGGATGGACGAGAACCCCCTGAACTATAGCAACTGGCGGCCCGGGGAGCCCAACAA 110
                                                      645 TGCTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCC 704
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APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REPERRENCE: AL-5
CURRENT APPLICATION NUMBER: 08/09/535,521
CURRENT FILING DATE: 1099-03-24
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 133
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APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL CANINE LOW APPLINTY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINE LOW NUCLEIC ACID MOLECULES AND USES THEREOF
TITLE REPREBURE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT APPLICATION NUMBER: 60/125,913
EARLIER PFILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
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57.7%; Pred. No. 4e-10;
tive 0; Mismatches 82; Indels
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; Patent No. 6410714
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                                                                                                                                                                705 CIGCICCACCICCC 718
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US-09-535-521-13
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LOCATION: (1)
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US-09-535-521-13
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Patent No. 6410714
Patent No. 6410710:
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
APPLICANT: Weber, Eric R.
APPLICANT: McCall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: NOVER: 2000-03-24
ERRIER APPLICATION NUMBER: 60/125,913
EARLIER PILING DATE: 1999-03-24
EARLIER PILING DATE: 1999-03-24
EARLIER PILING DATE: 1999-03-24
EARLIER PILING DATE: 1999-03-24
EARLIER PILING DATE: 1999-03-24
EARLIER PILING DATE: 1999-03-24
              APPLICANT: MCCall, Catherine A.

TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)

TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REPERENCE: AL-5

CURRENT APPLICATION NUMBER: US/09/535,521

CURRENT FILING DATE: 2000-03-24

EARLIER FILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PATENTIN Ver. 2.1
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Pred. No. 4e-10;
0; Mismatches 82; Indels
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Best Local Similarity 57.7%; Pred. No. 4e-10;
Matches 112; Conservative 0; Mismatches 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.7%;
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (1)
US-09-535-521-10
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109 CGGGGGCCAGGGGCGAGGACTGCGTGATGATGAGGCTCGGGGCTGGGGCAGTGGAATGACGCCTT 50
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8.4%; Score 62.8; DB 4; Length 423;
Best Local Similarity 57.7%; Pred. No. 4e-10;
Matches 112; Conservative 0; Mismatches 82; Indels
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; LENGTH: 423
; TYPE: DNA
; ORGANISM: Canis familiaris
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Search completed: June 21, 2004, 19:07:32 Job time: 82 secs

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Sequence 3705, Ap Sequence 1, Appli Sequence 2, Appli Sequence 24, Appli Sequence 1710, Ap Sequence 107, Ap Sequence 11785, A Sequence 45, Appl Sequence 43, Appl Sequence 43, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl Sequence 41, Appl
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                                                                                                                                                                               June 21, 2004, 18:23:44; Search time 409 Seconds (without alignments) 8366.928 Million cell updates/sec
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1: cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

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5: cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

7: cgn2_6/ptodata/1/pubpna/USO9_PUBCOMB.seq:*

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15: cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*

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669	904-096-60-SD	10	m	7.6	57	43
2079,	US-09-954	σ	4732	•	57	42
e 97,	US-10-336-603A-9	12	681	•	58.6	41
2031,	US-09-954-456-2	σ	4778		60.2	40
3, 2	US-09-971-429B-3	10	935	•	61.4	39
6	US-10-336-603A-	12	752	•	61.4	38
ď	US-10-336-603A-9	12	1161		61.8	37
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Sequence 30, Appl		σ	2248	8.4	62.6	35
Sequence 2274, Ap	US-09-954-456-22	6	1410	12.7	94.6	34
Sequence 47, Appl		13	1313	•	94.6	33
27.	ט	0	221	12.8	92.6	32
Sequence 1, Appli	US-09-727-030C-1	13	140	13.4	100	31
Seguence 14616, A	י	σ	240		107.2	30
Seguence 1207, Ap	US-10-311-455-1207	15	5815	14.5	108	29
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1208,	US-10-311-455-1208	15	5815		112.4	C 27
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Sequence 56, Appl	070-41	13	1802	24.7	184.4	25
52,	-415A-5	13	1802		184.4	24
54,	070-415A-5	13	1802	24.7	184.4	23
52,	070-415A-5	13	1802		184.4	22
51,	10-070-41	13	1802	24.7	184.4	21
50,	-10-070-415A-5	13	1802		184.4	20
	070-415A-4	13	1802	24.7	184.4	19
47,	10-070-415A-4	13	1802		184.4	18
equence 46,	US-10-070-415A-46	13	1802		•	17
44,	10-070-415A-4	13	1802		185	16
43,	-4	13	1802	24.8	ω	15

## ALIGNMENTS

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WS-10-164-536-2

Sequence 2, Application US/10054536

Sequence 2, Application US/10054536

Sequence 2, Application No. US20030162248Alutaka

Jublication No. US20030162248Alutaka

TITLE OF INVENTION: RECOMBINANT HUMAN MANNAN-BINDING PROTEINS AND PROCESS

TITLE OF INVENTION: FOR PRODUCING THE SAME

FILE REFERENCE: 19036/36614

CURRENT PAPLICATION NUMBER: US/10/054,536

CURRENT FILING DATE: 1908-07-23

PRIOR APPLICATION NUMBER: PCT/JP98/03311

PRIOR APPLICATION NUMBER: JP 10-11864

PRIOR PELING DATE: 1998-01-23

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PALENTING DATE: 1998-01-23

LENGTH: 747
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US-10-054-536-2
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Fatent No. US20020142981A1
FAPRICANT: NRORMATION:
APPLICANT: Vockley, Joseph G.
APPLICANT: Scherf, Uwe
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer;
FILE REFERENCE: 44921-5028-WO
CURRENT APPLICATION NUMBER: US 60/211,379
FRIOR APPLICATION NUMBER: US 60/211,379
FRIOR FILING DATE: 2000-06-14
FRIOR FILING DATE: 2000-10-02
FRIOR FILING DATE: 2000-10-02
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3705
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US-09-880-107-3705
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100.0%; Score 747; DB 9; Length 3605;
Best Local Similarity 100.0%; Pred. No. 4.5e-236;
Matches 747; Conservative 0; Mismatches 0; Indels 0
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Sequence 1, Application US/10054536

Sequence 1, Application US/10054536

Sequence 1, Application US/2030162248A1

GENERAL INFORMATION:

APPLICANT: WAKAMIYA, No. US20030162248A1utaka

TITLE OF INVENTION: FOR PRODUCING THE SAME

TITLE OF INVENTION: FOR PRODUCING THE SAME

FILE REFERENCE: 19036/36614

CURRENT APPLICATION NUMBER: US/10/054,536

CURRENT PILING DATE: 1998-07-23

PRIOR FILING DATE: 1998-07-23

PRIOR FILING DATE: 1998-01-23

PRIOR FILING DATE: 1998-01-23

NUMBER OF SEQ ID NOS: 28

SOFTWARE: PATCHIN UVE: 2.0

LENGTH: 3605
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APPLICANT: Mao, Mao
APPLICANT: Linsley, Peter S
APPLICANT: Linsley, Peter S
APPLICANT: Lund, Lund
TITLE APPLICANT: Lund, Lund
CINEMAL APPLICATION NUMBER: US/10/429,160
CURRENT APPLICATION NUMBER: US/10/429,160
CURRENT FILING DATE: 2003-05-02
PRIOR PILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 111
SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
LINGTH: 3605
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Best Local Similarity 100.
Matches 747; Conservative
                                                                                                                                              TYPE: DNA
CORGANISM: Homo sapiens
US-10-429-160-57
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100.0%; Pred. No. 4.5e-236;
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Matches 747; Conservative
   ; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (66)..(809)
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; NAME/KEY: mat_peptide
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US-10-054-536-1
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                                                                                                                                                                                                                                                                      186 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAGGGG
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                                                                                                                                                                                                                                                                                                                                                  246 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC
                                                                                                                                                                                     126 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AATCCAGGCCTTCTGGGTCACCAGGACCAAAGGCCAAAAAGGAGACCTGGAAAAAGT
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                                                                                1 ATGICCCIGITICCATCACTCCCTCTCTCTCTGAGTATGGTGGCAGCGTCTTACTCA
                                                                                                                                                                GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT
                                            Gaps
                                        0
Length 3605;
                                          Indels
  100.0%; Score 747; DB 17;
100.0%; Pred. No. 4.5e-236;
iive 0; Mismatches 0;
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Sequence 57, Application US/10429160; Publication No. US20040023276Al GENERAL INFORMATION; APPLICANT WAYA

RESULT 4 US-10-429-160-57

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AGCICICCAGGCAICAACGGCIICCCAGGCAAAGAIGGGCGIGAIGGCACCAAGGGAGAA 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 ATGCCACGTATCAAAAGTGGCTGACCTTCTCTCTGGCAAACAAGTTGGGAACAAGTTC 414
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                                                                                                                                                                                                                        APPLICANT: Hang, Ning
APPLICANT: Rodrguez, Raymond
APPLICANT: Rodrguez, Raymond
APPLICANT: Rodrguez, Raymond
TITLE OF INVENTION: Feed Additive Compositions and Methods
TITLE OF INVENTION: Feed Additive Compositions and Methods
CURRENT APPLICATION NUMBER: US/10/076,816
CURRENT FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/269,188
PRIOR APPLICATION NUMBER: US 09/847,232
PRIOR PILING DATE: 2001-05-02
PRIOR PILING DATE: 2001-05-02
PRIOR PELING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
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PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
PRIOR FILING DATE: 2001-05-02
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 444.6; DB 15; Length
Pred. No. 4.1e-136;
0; Mismatches 169; Indels
                        661 CTGGCCGTCTGTGAGTTCCCTATC 684
                                                                                                                                                            ; Sequence 54, Application US/10076816; Publication No. US20030056244A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 59.5%;
Best Local Similarity 76.4%;
Matches 575; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Bos taurus
                                                                                                                                      US-10-076-816-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: BO
US-10-076-816-54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA
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                                                                                                                        TITLE OF INVENTION: Anticancer agent
TITLE OF INVENTION: Anticancer agent
FILE REFERENCE: ADT 308
CURRENT APPLICATION NUMBER: US/09/971,475
CURRENT FILING DATE: 2001-10-04
PRIOR PILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 09/468,705
PRIOR FILING DATE: 1998-08-19
PRIOR APLICATION NUMBER: DF 239113/97
PRIOR APLICATION NUMBER: JF 239113/97
PRIOR PILING DATE: 1997-08-21
SPRIOR FILING DATE: 1997-08-21
SOFTWARE: Patentin Ver: 2.0
SOFTWARE: Patentin Ver: 2.0
                                                         Sequence 2, Application US/09971475
Publication No. US20020086817A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo Bapiens US-09-971-475-2
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                                                                                                            304
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| Sublication No. US20040005547A1
| GENERAL INFORMATION:
| APPLICANT: Boess, Franziska
| APPLICANT: Boess, Franziska
| APPLICANT: Wolf, Detlef
| TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
| TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
| TITLE OF INVENTION: BIOMARKERS AND EXPRESSION PROFILES FOR TOXICOLOGY
| TITLE OF ILING DATE: 2003-03-14
| CURRENT FILING DATE: 2003-03-14
| PRIOR APPLICATION NUMBER: 02015657.6
| PRIOR PILING DATE: 2002-03-14
| PRIOR PILING DATE: 2002-03-14
| PRIOR PILING DATE: 2002-03-14
| PRIOR PILING DATE: 2002-03-14
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           AAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTG
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US-09-917-800A-1710
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TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 4921-5018-US
CURRENT APPLICATION UMBER: US/09/917,800A
CURRENT FILING DATE: 2001-07-31
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PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 60/222,040
PRIOR APPLICATION NUMBER: US 60/222,080
PRIOR APPLICATION NUMBER: US 60/290,029
PRIOR FILING DATE: 2001-05-11
PRIOR FILING DATE: 2001-05-15
PRIOR PELING DATE: 2001-05-15
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PRIOR PLILING DATE: 2001-06-19
PRIOR FILING DATE: 2001-06-19
PRIOR PRIOR PAPELICATION NUMBER: US 60/293,459
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Patent No. US20020119462A1
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APPLICANT: Castle, Arthur
APPLICANT: Blashoff, Michael
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APPLICANT: Mendrick, Donna
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APPLICANT: HASHIMOTO, Michie

APPLICANT: ASHIMOTO, Michie

APPLICANT: MISHINO

APPLICANT: MISHINO

TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE

FILE REFERENCE: 22063JUSSERDET

CURRENT APPLICATION NUMBER: US/10/070,415A

CURRENT PILING DATE: 2003-03-05

PRIOR APPLICATION NUMBER: US/2001-090053

PRIOR PILING DATE: 2001-03-05

PRIOR FILING DATE: 2001-09-18

PRIOR FILING DATE: 2001-09-18

NUMBER OF SEQ ID NOS: 72

SOFTWARE: PATENTIN VUMBER: 37

SEQ ID NO 45

LENGTH: 1802

LENGTH: 1802
                                                        148 GGTCCTCCGGGCATCAATGGCATCCCAGGCAAAGATGGGCGTGATGGTGCCAAGGGAGAA
                                                                                                                                   208 AAGGAGAAAACCAGGTCAAGGACTCAGAGGCTCGCAGGGCCCCCTGGAAAGATGGGGCCCT
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                         115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAA
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: OTHER INFORMATION: n is a nucleotide selected from a,

US-10-070-415A-45A
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NAME/KEY: misc_feature
LOCATION: (649)...(649)
OTHER INFORMATION: n is a nucleotide selected from
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; Sequence 45, Application US/10070415A
; Publication No. US20040043379A1
; GENERAL INFORMATION:
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NAME/KEY: misc feature
LOCATION: (884)...(884)
OTHER INFORMATION: n is a 1
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OTHER INFORMATION: n is a
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Best Local Similarity 98.9
Matches 186; Conservative
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NAME/KEY: misc feature
LOCATION: (868)..(868)
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ORGANISM: Homo sapiens
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Patent No. US20020137139A1
GENERAL INFORMATION:
APPLICANT: Harren, Wesley C.
APPLICANT: Harren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
APPLICANT: Byatt, John C.
APPLICANT: Harren, Wasley C.
APPLICANT: MATHIALAGAN, NAGAPPAN
TITLE OF INVENTION: NUCLEIC AID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298) C
CURRENT PILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 11785
LENGTH 4.0
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; OTHER INFORMATION: Clone ID: 50-LIB34-061-Q1-E1-E6
US-09-960-352-11785
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Pred. No. 1.2e-62;
0; Mismatches 75;
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Best Local Similarity 78.3%;
Matches 307; Conservative C
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835 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGNCACCAAGGNAGAAAAGGG 894
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NAME/KRY: misc_feature
LOCATION: (875)..(875)
OTHER INFORMATION: n is a nucleotide selected from a, g, c,
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LOCATION: (649)...(649)
OTHER INFORMATION: n is a nucleotide selected from
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LOCATION: (96)...(96)
OTHER INFORMATION: n is a nucleotide selected from
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OTHER INFORMATION: n is a nucleotide selected from
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NAME/KEY: misc feature
LOCATION: (868)..(868)
OTHER INFORMATION: n is a nucleotide selected from
                                                                                                                                                                                                                                            US-10-070-415A-53; Sequence 53, Application US/10070415A; Publication No. US20040043379A1
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Best Local Similarity 98.9
Matches 186; Conservative
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ORGANISM: Homo sapiens
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APPLICANT: HASHIMOTO, Michie
APPLICANT: ASHIMOTO, Michie
APPLICANT: ASHIMOTO, Michie
APPLICANT: OTPA, Yasuhiko
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
FILE REFERENCE: 220633US2SRDPCT
CURRENT APPLICATION NUMBER: D03-07-23
PRIOR APPLICATION NUMBER: PCT/JP02/0230
PRIOR FILING DATE: 2002-03-05
PRIOR PLING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: JP 2001-090053
PRIOR APPLICATION NUMBER: JP 2001-284112
PRIOR APPLICATION NUMBER: JP 2001-284112
PRIOR APPLICATION NUMBER: JP 2001-284112
SPRIOR PRIOR APPLICATION NUMBER: JP 2001-284112
SPRIOR APPLICATION NUMBER: JP 2001-09-18
SOFTWARE: Patentin version 3.1
                              715 ATGTCCCTGTTTCCATCACTCCCTCTCCTTGTATGGTGGCGCGCGTTTACTCC
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; LOCATION: (875)...(875)
; OTHER INFORMATION: n is a nucleotide selected from a, g,
US-10-070-415A-49
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NAMB/KEY: misc_feature
LOCATION: (425)...(425)
OTHER INFORMATION: n is a nucleotide selected from a,
FEATURE:
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LOCATION: (649)...(649)
OTHER INFORMATION: n is a nucleotide selected from a,
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OTHER INFORMATION: n is a nucleotide selected from a,
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OTHER INFORMATION: n is a nucleotide selected from
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Pred. No. 2.1e-50;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                          Sequence 49, Application US/10070415A Publication No. US20040043379A1
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98.9%;
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Best Local Similarity 98.9<sup>5</sup>
Matches 186; Conservative
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NAME/KEY: misc_feature
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US-10-070-415A-49
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US-10-070-415A-42
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835 CCAGGCATCAACGCTTCCCAGGCAAAGATGGGNGTGATGNCACCAAGGGAGAAAAGGGG 894
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APPLICANT: ASHIMOTO, Michie
APPLICANT: MISHIRO, Shunji
APPLICANT: MISHIRO, Shunji
APPLICANT: OOTA, Yasuhiko
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
FILE REFRENCE: 220333USZSRDPCT
CURRENT APPLICATION NUMBER: US/10/070,415A
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Pred. No. 4.4e-50;
0; Mismatches 3; Indels 0
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incarion: (884)
CTHER INFORMATION: n is a nucleotide selected from a, g, c,
US-10-070-415A-41
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NAME/KEY: misc_feature
LOCATION: (875)..(875)
OTHER INFORMATION: n is a nucleotide selected from a,
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OTHER INFORMATION: n is a nucleotide selected from a,
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NAMBYKEY:
LOCATION: (868)...(868)
OTHER INFORMATION: n is a nucleotide selected from
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PRIOR APPLICATION NUMBER: PCT/JP02/02030
PRIOR FILING DATE: 2002-03-05
PRIOR PLILING DATE: 2002-03-05
PRIOR PLILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: JP 2001-090053
PRIOR APPLICATION NUMBER: JP 2001-284112
PRIOR APPLICATION NUMBER: JP 2001-284112
PRIOR APPLICATION NUMBER: JP 2001-284112
SOFTWARE: PATENTIN VERSION 3.1
                                                                                                                                                                   Sequence 41, Application US/10070415A Publication No. US20040043379A1 GENERAL INFORMATION:
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Best Local Similarity 98.4%;
Matches 185; Conservative 0
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OTHER INFORMATION: n is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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                                   181 GAACCAGG 188
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895 GAACCAGG 902
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715 ATGICCCTGTTTCCATCACTCCCTCTCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA 774 61 GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120 121 CCAGGCATCAACGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAGGG 180 835 CCAGGCATCAACGCCTTCCCAGGCAAAGATGGGNGTGATGNCACCAAGGNAGAAAAGGGG 894 APPLICANT: HASHIMOTO, Koji

APPLICANT: ASHIMOTO, Michie

APPLICANT: ASHIMOTO, Michie

APPLICANT: MISHIMOTO, Michie

APPLICANT: MISHIMOTO, Michie

APPLICANT: OTRY, Yasuhiko

TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE

FILE REFERENCE: 220633USZSRDPCT

CURRENT APPLICATION NUMBER: PCT/JP02/02030

PRIOR FILING DATE: 2002-03-05

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-27

PRIOR FILING DATE: 2001-03-18

SOFTWARE: PLICATION NUMBER: JP 2001-204112

NUMBER OF SEQ ID NOS: 72

SEQ ID NO 42

LENGTH: 1802 1 ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCTGAGTATGGTGGCAGCGTCTTACTCA Gaps 0; or ö ö or or Score 185; DB 13; Length 1802; Pred. No. 4.4e-50; 0; Mismatches 3; Indels 0 NAME/KEY: misc feature LOCATION: (884)..(884) OTHER INFORMATION: n is a nucleotide selected from a, g, c, ΰ ນ້ ΰ δ ģ ģ 6 ď LOCATION: (96)...(96)
OTHER INFORMATION: n is a nucleotide selected from a, FEATURE:
MAMB/KEY: misc\_feature
LOCAFICON: (649). (649).
OTHER INFORMATION: n is a nucleotide selected from NAME/KEY: misc feature LOCATION: (868)..(868) OTHER INFORMATION: n is a nucleotide selected from NAME/KEY: misc feature LOCATION: (875)..(875) OTHER INFORMATION: n is a nucleotide selected from ; Sequence 42, Application US/10070415A; Publication No. US20040043379A1; GENERAL INFORMATION: Query Match
Best Local Similarity 98.4%;
Matches 185; Conservative TYPE: DNA ORGANISM: Homo sapiens NAME/KEY: misc feature GAACCAGG 188 GAACCAGG 902

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RESULT 15 US-10-070-415A-43 ; Sequence 43, Application US/10070415A

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Publication No. US20040043379A1

GENERAL INFORMATION:
APPLICANT: HASHIMOTO, Koji
APPLICANT: ASHIMOTO, Michie
APPLICANT: ASHIMOTO, Michie
APPLICANT: MISHIRO, Shunji
APPLICANT: MISHIRO, Shunji
APPLICANT: OTIA, Yasuhiko
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID ASSOCIATED WITH DISEASE
FILE REFRENCE: 220633US2SRDPCT
CURRENT FILING DATE: 2003-07-23
PRIOR PELICATION NUMBER: US/10/070,415A
CURRENT FILING DATE: 2003-07-23
PRIOR APPLICATION NUMBER: UP 2001-09053
PRIOR PLING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-18
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Patentin version 3.1
SEQ ID NO 43
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NAME/KEY: misc feature
LOCATION: (884)
CHER INFORMATION: n is a nucleotide selected from a, g, c, or US-10-070-415A-43
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OKGANISM: Homo sapiens
FERTURE:
NAME/KEY: misc_feature
COCATION: (96)...(96)
OTHER INFORMATION: n is a nucleotide selected from a, g, FERTURE:
NAME/KEY: misc feature
LOCATION: (649)...(649)
OTHER INFORMATION: n is a nucleotide selected from a, g, FERTURE:
NAME/KEY: misc feature
LOCATION: (868)...(868)
OTHER INFORMATION: n is a nucleotide selected from a, g, OTHER INFORMATION: n is a nucleotide selected from a, g, OTHER INFORMATION: n is a nucleotide selected from a, g,
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LOCATION: (875)..(875)
OTHER INFORMATION: n is a nucleotide selected from a, g,
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Search completed: June 21, 2004, 20:12:09 Job time : 412 secs

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ascaris suu gallus gall mus musculu

P27393 P32018

ASCSU HUMAN BOVIN HUMAN

CA24\_; CA1E\_( CA44\_] TETN PGCB\_ C10B

homo sapien gallus gall mus musculu

P53420 P05452 Q28062 P02746 P320145 P02745 Q07643 Q02105 Q02105 Q089218 Q14055

C1QA\_HUMAN CA39\_CHICK CA29\_MOUSE

C1QC\_HUMAN C1QC\_MOUSE KF10\_HUMAN CA12\_MOUSE CA29\_HUMAN

homo sapien mus musculu

homo sapien mus musculu homo sapien

ALIGNMENTS

mus musculu mus musculu homo sapien

Q9wts8 Q15848 Q60994 P98086 Q01955

rattus norv rattus norv homo sapien

PSPA\_PIG PSPA\_CANFA CLEI HUMAN FCE2\_MOUSE CLOB MOUSE CLOB RAT APMI MOUSE CLOB RAT APMI MOUSE CLOB M

homo sapien mus musculu mus musculu

gallus gall

P06908 075596 P20693 P02707 P14106

canis famil

us-10-054-536-2.rsp

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 Command line parameters:
-MODEL=frame+ n2P.model -DEV=xlp
-MODEL=frame+ n2P.model -DEV=xlp
-DE-cgn2 1/USFTO_spool p/US10054536/runat_18062004 173455 13573/app_query.fasta_1.903
-DB=SwissProt 42 -QFMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LGOPCL=0 -LGOPEXT=0
-DB=SwissProt 42 -QFMT=fastan -SUFFIX=rsp -MINMATCH=0.1 -LGOPCL=0 -LGOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS-human40.cdi -LIST=45
-UNITS=bits -START=1 -END=-1 -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFWT=pto -NORN=ext -HEAPSIZE=50 -MINLEN-0 -MAXIEN-200000000
-USFR=EXS10054536 @CGN 1 1 16 @runat 18062004 173455 13573 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG-SCORES=0 -MAIT -DSFBLOCK=100 -LONGLOG
-DOWNAPP -LARGEQUERY -NEG-SCORES=0 -THRRANS=1 -XGAPCP=10 -XGAPEXT=0.5 -FGAPCP=6
-DEGAPEXT=7 -YGAPCP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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002659 bos taurus
P41317 mus musculu
                                                                                                               ; Search time 15 Seconds
(without alignments)
5186.187 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                using frame_plus_n2p model
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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rattus norv homo sapien bos taurus

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rattus norv mus musculu oryctolagus bos taurus

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rattus norv mus musculu

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bos taurus

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257.9 257.5 257.5 257.5 257.5 257.5 257.5 258.6

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bos taurus

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MEDLINE=93265124; PubMed=1303250; Super M., Gillies S.D., Foley S., Sastry K., Schweinle J.E., Silverman V.J., Ezekowitz R.A.; "Distinct and overlapping functions of allelic forms of human mannose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91269930; PubMed=1675710;
Sumiya M., Super M., Tabona P., Levinsky R.J., Arai T., Turner M.W.,
Summarfield J.A.,
"Molecular basis of opsonic defect in immunodeficient children.";
Lancet 337:1569-1570([991].
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Gabolde M., Maralitharan S., Besmond C.;
Gabolde M., Maralitharan S., Besmond C.;
Gabolde M., Maralitharan S., Besmond C.;
Genctyping of the three major allelic variants of the human mannose-binding lectin gene by denaturing gradient gel electrophoresis.";
Hum. Matat. 14:80-83(199).
-!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-dependent manner. Is capable of host defense against pathogens, by activating the classical complement pathway independently of
"Different molecular events result in low protein levels of mannan-binding lectin in populations from South-East Africa and South America.";
                                                                                                                                                      of mannan-binding lectin cDNA of Chinese.";
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-59 FROM N.A., AND VARIANT ASP-54.
MEDLINE=22167090; PubMed=12175909;
Jueliger S., Kremener P.G., Alpers M.P., Reeder J.C., Kun J.F.J.;
"Restricted polymorphisms of the mannose-binding lectin gene in a population of Papua New Guinea.";
                                                                                                                                                                                                                          TISSUB-Liver, and Plasma; MEDLINE=95073978; PubMed=7982896; Kurata H., Sannoh T., Kozutsumi Y., Yokota Y., Kawasaki T.; "Structure and function of mannan-binding proteins isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANTS ASP-54 AND GLU-57.
MEDLINES-9258313; PubMed=1304173;
Lipscombe R.J., Sumiya M., Hill A.V.S., Lau Y.L., Levinsky R.J.,
Summerfield J.A., Turner M.W.;
"High frequencies in African and non-African populations of
independent mutations in the mannose binding protein gene.";
Hum. Mol. Genet. 1:709-715(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lipscombe R.J., Sumiya M., Hill A.V.S., Lau Y.L., Levinsky R.J., Summerfield J.A., Turner M.W.; Hum. Mol. Genet. 2:342-342(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 108-248.
MEDLINE=95360730; PubMed=7634089;
Sheriff S., Chang C.Y., Ezekowitz R.A.;
Human mannose-binding protein carbohydrate recognition domain trimerizes through a triple alpha helical coiled-coil.";
Nat. Struct. Biol. 1:789-794(1994).
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SUBUNIT: Oligomeric complex of 6 set of homotrimers.
                                                                                               SEQUENCE FROM N.A., AND VARIANT ALA-24
                                                                                                                               Chen Z., Zhu X., Xie P.;
"Cloning and sequencing of mannan
Mian Yi Xue Za Zhi 15:83-86(1999)
                                                                                                                                                                                                                                                                                                             J. Biochem. 115:1148-1154 (1994).
                                                         Immunol. 161:3169-3175(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DR GO; GO: 0005615; -: C: extracellular space; TAS.

DR GO; GO: 0005615; P: immune response; TAS.

DR GO; GO: 0006955; P: immune response; TAS.

DR InterPro; IPR001304; Lectin_C.

DR Pfam; PF01391; Collagen; 1.

DR Pfam; PF00191; Collagen; 1.

DR Pfam; PF01059; lectin_C; 1.

DR Pfam; PF00191; CIECTIN_C; 1.

DR PROSITE; PS00615; C TYPE LECTIN 1; 1.

DR PROSITE; PS00615; C TYPE LECTIN 2; 1.

DR PROSITE; PS00615; C TYPE LECTIN 2; 1.

RW Complement pathway; Membrane; Mannose-binding; Calcium; Repeat; KW Signal; Collagen; Lectin; Glycoprotein; Hydroxylation; Polymorphism; KW 3D-structure.

TR SIGNAL 1.
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/FTd=vAR 013294.

FTd=vAR 013294.

F 0.054 of European and African populations; dbSNP:5030737).

/FTd=vAR 08543.

/FTd=vAR 08543.

/FTd=vAR 0804545.

/FTd=vAR 0804182.

dbSNP:1800451).
-i- DISEASE: There is an association between low levels of MBL2 and a defect of opsonization which results in susceptibility to frequent and chronic infections.
-i- SIMILARITY: Contains 1 collagenous domain.
-i- SIMILARITY: Contains 1 C-type lectin famility domain.
-i- CAUTION: There are extensive differences between the revised sequence in Ref.1 and that published in Ref.2.
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Li, X1554; CAA34079.1;
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Li, X15555; CAA34079.1;
Li, X15555; CAA34079.1;
JOINED.
ABL, X15556; CAA34079.1; JOINED.
ABL, AF080510; AAC31937.1;
LEMBL, AF080509; AAC31937.1;
LEMBL, Y16576; CAB56044.1;
LEMBL, Y16576; CAB56044.1;
LEMBL, Y16579; CAB56120.1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-97228413; PubMed-9074491;
Kawai T., Suzuki Y., Bda S., Ohteni K., Kase T., Pujinaga Y.,
Sakamoto T., Kurimura T., Wakamiya N.;
"Cloning and characterization of a cDNA encoding bovine mannan-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- FUNCTION: Binds mannose and N-acetylglucosamine in a calciumdependent manner. Is capable of host defense against pathogens, b activating the classical complement pathway independently of the antibody (By similarity).
-!- SUBBUNIT: Oligomeric complex of 6 set of homotrimers.
-!- SIMILARITY: Contains 1 collagenous domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                  MABC_BOVIN STANDARD; PRT; 249 AA.
002659;
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mannose-binding protein C precursor (MBP-C) (Mannan-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR008161; Clg helix.

R InterPro; IPR008161; Clg helix.

R InterPro; IPR001304; Lectin C.

R Fam; PF01391; Collagen; I.

R Probom; PF000007; Clg_helix; I.

R SMART; SM00004; ClgChelix; I.

R SMART; SM00014; ClrgF_LECTIN I; I.

R PROSITE; PS00641; CTYPE_LECTIN I; I.

R Complement pathway; Membrane; Mannose-binding; Calcium; Repeat;

R Signal; Collagen; Lectin; Glycoprotein; Hydroxylation.

T GIGNAL

T CHAIN

21 249 MANNOSE-BINDING PROTEIN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Evkaryota; Metazooa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLLAGEN-LIKE.
C-TYPE LECTIN
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
INTERCHAIN (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
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EMBL; D73408; BAA18935.1; -. HSSP; P11226; 1HUP.
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us-10-054-536-2.rsp

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U09013; AAAB2010.1; JOINED. U09014; AAAB2010.1; JOINED.
NCBI_TaxID=10090;
                                                                                                                           Sastry K.
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EMBL;
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                                                                                  21 AspThrGluThrGluAsnCysGluAsnIleArgLysThrCysPro---ValIleAlaCys
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ThrGlyUysGlyValThrTyrGlnAsnTrpAsnAspGlyGluProAsnAsnAlaSerPro
                                                                                                                                            115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCCACCAAGGGAGAA
                                                                                                                                                       GlyProProGlyIleAsnGlyIleProGlyLysAspGlyArgAspGlyAlaLysGlyGlu
                                                                                                                                                                                         CCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGCCCTGGA
                                                                                                                                                                                                                                                                      GluAsnMetGlyAspTyrIleArgLeuAlaThrSerGluArgAlaThrLeuGlnSerGlu
                                                                                                                                                                                                                                                                                       355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTC
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                                                                        ATGTCCCTGTTTCCATCACTCCCTCCTTCCTCCTGAGTATGGTGGCGCCTCTTACTCA
                                                                                                          TGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGT
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                                                                                                                                                                                                                                                     TTCCTGACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAAGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Mannan-binding protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBL2.
Was musculus (Mouse).
Bukar musculus (Hordaca; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                ::
 161
27
59
3
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
nonose-binding protein C precursor (MBP-C) (KRA-reactive factor P28A subunit) (RARF/P28A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCCCATCTGGCCGTCTGTGAGTTCCCTATC 744
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                             Indels:
                                     Gaps:
                                                      US-10-054-536-2 (1-747) x MABC_BOVIN (1-249)
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                                                                                                         GAAACTGTGACC----
847.50
75.20%
64.40%
62.09%
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                 Best Local Similarity:
Query Match:
         Similarity:
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P41317;
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between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MEDLINE=22388257; PubMed=12477932;

MA Stausher R.D., Felingold E.A., Grouse L.H., Derge J.G.,

MA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

MA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarane P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Yillalon D.K., Muxny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Halton B., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

M. Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBGULT: Oligomeric complex of 6 set of homotrimers.
SUBCELLULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MOST
BEEDOMINANTLY IN THE ROUGH ENDOPLASMIC RETICULON AND IN THE GOLGI
APPRARTUS, AND LITTLE ON OMB IS PRESENT IN PLASMA MEMBRANES AND
LYSOSOMES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNAL
SPACE OF THE ORGANELLES, PROBABLY AS A LOOSELY BOUND MEMBRANE
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                                                                                  MEDLINE-91302823; PubMed=1712818; Sastry K., Zahedi K., Lelias J.M., Whitehead A.S., Ezekowitz R.A.; Molecular characterization of the mouse mannose-binding proteins. The mannose-binding protein A but not C is an acute phase reactant."; J. Immunol. 147:692-697(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-dependent manner. Is capable of host defense against pathogens, b activating the classical complement pathway independently of the
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                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=BALB/C;
MEDLINE=95284466; PubMed=7766991;
Sastry R., Wang J.S., Brown D.C., Ezekowitz R.A., Tauber A.I.,
Sastry K.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ihara S., Watanabe E., Watanabe M., Takishima K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kuye S., Ihara S., Watanabe E., Watanabe M., Takishima K
Mamaiya G., Kawakami M.,
Submitted (UU-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C-type lectin family domain.
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EMBL; U09016; AAA82010.1; -.
                                                STRAIN=CBA/J; TISSUE=Liver;
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SEQUENCE FROM N.A.
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| GluLeuArgAlaLeuArgAsnTrpValLeuPheSerLeuSerGluLysValGlyLysLys
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                                                                                                                                                                                                   Complement pathway; Membrane; Mannose-binding; Calcium; Repeat;
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                                                                                                                                                                                                                                                            COLLAGEN-LIKE.
C-TYPE LECTIN.
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (BY SIMILARITY).
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
I -> L (IN REF. 1).
V -> A (IN REF. 1).
W, 49AE84E2290DEBOA CRC64;
                                                                                                                                                                                                                                                  MANNOSE-BINDING PROTEIN C
                                                                                                                                                                                                                 Signal, Collagen, Lectin, Glycoprotein, Hydroxylation SIGNAL 1 18 BY SIMILARITY.
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                                                                                                                 Pfam; PF01391; Collagen; 1.
Pfam; PF00159; Collagen; 1.
SMART; SM000134; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE_LECTIN 2; 1.
U09015; AAA82010.1; JOINED.
D11440; BAA02005.1; -.
                                                                       MGD; MGI 96924; Mbl2.
InterPro; IPR008160; Collagen.
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PIR; 148651; LNMSMC.
HSSP; P08661; 1RDO.
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                                                                                                          ATCAAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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Oka S., Itoh N., Kawasaki T., Yamashina I.;
"Primary structure of rat liver mannan-binding protein deduced from its cDNA sequence.";
J. Biochem. 101:135-144(1987).
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J. Biol. Chem. 271:663-674(1996).
-!- FUNCTION: Binds mannose and N-acetylglucosamine in a calciumdependent manner. Is capable of host defense against pathogens activating the classical complement pathway independently of t
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01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
14-MAR-2004 (Rel. 43, Last annotation update)
(RA-reactive factor P28A subunit) (RARF/P28A)
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MEDLINE=96132792; PubMed=8557671;
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J. Biol. Chem. 261:6878-6887(1986)
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                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
PREDOMINANTLY IN THE ROUGH ENDOPLASMIC RETICULUM AND IN THE GOLGI APPARATUS, AND LITTLE OR NO MBP IS PRESENT IN PLASMA MEMBRANES AND LYSOSOMES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNAL SPACE OF THE ORGANELLES, PROBABLY AS A LOOSELY BOUND MEMBRANE
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Complement pathway; Membrane; Mannose-binding; Calcium; Repeat;
Signal; Collagen; Lectin; Glycoprotein; Hydroxylation; 3D-structure.
SIGNAL 1
                                                                                  SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C-type lectin family domain.
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EMBL; X05023; CAA28687.1; --
FIR; A24791; LINRTMC.
PDB; IRD1; 08-MAR-96.
PDB; IRD1; 08-MAR-96.
PDB; IRD5; 08-MAR-96.
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PDB; IRD5; 08-MAR-96.
PDB; IRC8; 08-MAR-96.
PDB; IRC8; 05-UUL-02.
PDB; IRC2; 05-UUL-02.
PDB; IRC2; 05-UUL-02.
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InterPro; IPR001304; Lectin_C.
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                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mannose-binding protein A precursor (MBP-A) (Mannan-binding protein)
 F0706E2AA9331531 CRC64;
                                           244
151
34
57
57
                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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26014 MW;
                                           9.47e-58
785.00
75.20%
61.38%
57.51%
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EMBL;
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                                                                                                                                                                    SEQUENCE
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DB:
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MABA_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: Oligomeric complex of 6 set of homotrimers.
SUBCELLULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MOST
PREDOMINANTLY IN THE ROUGH ENDOPLASMIC RETICULUM AND IN THE GOLGI
APPARATUS, AND LITTLE OR NO MBP PRESENT IN PLASMA MEMBRANES AND
LYSOSOMES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNAL
SPACE OF THE ORGANELLES, PROBABLY AS A LOOSELY BOUND MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ρχ
                                                                                                                                                                                                                                      MEDLINE=91302823; PubMed=1712818; Sastry K., Zahedi K., Lelias J.M., Whitehead A.S., Ezekowitz R.A.; Medecular characterization of the mouse mannose-binding proteins. The mannose-binding protein A but not C is an acute phase reactant."; J. Immunol. 147:692-697(1991).
reactive factor polysaccharide-binding component P28B polypeptide)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of murine mannose-binding protein genes Mbll and Mbl2 reveals features common to other collectin genes.";
Mamm. Genome 6:103-110(1995).
--- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-dependent manner. Is capable of host defense against pathogens, activating the classical complement pathway independently of the
                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=BALB/C; TISSUE=Liver; MEDLINE=22345256; PubMed=1637628; MEDLINE=22345256; PubMed=1637628; Kuge S., Ihara S., Watanabe E., Watanabe M., Takishima K., Suga T., Mamiya G., Kawakami M.; "cDNAs and deduced amino acid sequences of subunits in the binding component of mouse bactericidal factor, Ra-reactive factor: similarity to mannose-binding proteins."; Biochemistry 31:6943-6950(1992).
                                                                                                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Complement pathway; Membrane; Mannose-binding; Calcium; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-95284466; PubMed-7766991;
Sastry R., Wang J.S., Brown D.C., Ezekowitz R.A., Tauber A.I.
Sastry K.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 collagenous domain.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
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EMBL; U09007; AAA82009.1; JOINED.
EMBL; U09008; AAA82009.1; JOINED.
EMBL; U09009; AAA82009.1; JOINED.
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InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin_C.
                                                                    Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D11441; BAA02006.1; -. S42292; AAB19342.1; -.
                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CBA/J; TISSUB=Liver;
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                                                                                                                                                                                                                                                                                                                                              J. Immunol. 147:69
[2]
SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody.
                         P28B)
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240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        150 GlnGlyThrValAlaIleProArgAsnAlaGluGluAsnLysAlaIleGlnGluValAla
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                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein; Hydroxylation.
BY SIMILARITY.
MANNOSB-BINDING PROTEIN A.
COLLAGEN-LIKE.
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                          D222F1A748D424D9 CRC64;
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144
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63
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                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
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57.83%
52.12%
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       Lectin;
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   Signal; Collagen; SIGNAL 1
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37
144
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THE ORGANELLES, PROBABLY AS A LOOSELY BOUND MEMBRANE PROTEIN.
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2MSB; 31-OCT-93.
1AFA; 03-APR-96.
1AFB; 03-APR-96.
1AFD; 03-APR-96.
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17-JUN-98.
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05-JUL-02.
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1KXO; 05-JUL-02
1KX1; 05-JUL-02
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1RTM;
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1FIH;
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1BCH;
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PDB;
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PDB;
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                                                                                                                                                                                                                                                                                                                            PDB;
   antibody.
SUBUNIT: Oligomeric complex of 6 set of homotrimers.
SUBCELLULAR LOCATION: THIS PROTEIN IS LOCATED INTRACELLULAR, MOST PREDOMINANTLY IN THE ROUGH ENDOPLASNIC RETICULM AND IN THE GOLGI APPARATUS, AND LITTLE OR NO MBP IS PRESENT IN PLASNA MEMBRANES AND LYSOSOMES. THE MBP IS EXCLUSIVELY LOCALIZED IN THE CISTERNAL SPACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                 01-FEB-1991 (Rel. 17, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Mannose-binding protein A precursor (MBP-A) (Mannan-binding protein),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92086855; PubMed=1721241;
Weis W.I., Kahn R., Fourme R., Drickamer K., Hendrickson W.A.;
"Structure of the calcium-dependent lectin domain from a rat mannose-binding protein determined by MAD phasing.";
Science 254:1608-1615(1991).
                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochemistry 37:17965-17976(1998).

-!- FUNCTION: Binds mannose and N-acetylglucosamine in a calcium-
dependent manner. Is capable of host defense against pathogens, k
activating the classical complement pathway independently of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87222353; PubMed=3584121; Ikeda K., Sannoh T., Kawasaki T., Yamashina I.; Sannoh T., Kawasaki N., Kawasaki T., Yamashina I.; Serum lectin with known structure activates complement through the classical pathway."; J. Biol. Chem. 262:7451-7454(1987).
                                                                                                                                                                                                                                                     Drickamer K., Dordal M.S., Reynolds L.,
"Mannose-binding proteins isolated from rat liver contain
carbohydrate-recognition domains linked to collagenous tails.
Complete primary structures and homology with pulmonary surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Exon structure of a mannose-binding protein gene reflects its evolutionary relationship to the asialoglycoprotein receptor and nonfibrillar collagens.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93063338; PubMed-1436090; Weis W.I., Drickamer K., Hendrickson W.A.; "Structure of a C-type mannose-binding protein complexed with an oligosaccharide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 90-238.
MEDLINE=99119227; PubMed=9922165;
NG K.K.-S., Park-Snyder S., Weis W.I.,
"Ca2+-dependent structural changes in C-type mannose-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 84-238.
MEDLINE=95219384; PubMed=7704532;
MEDLINE=192184: Drickamer K.;
"Trineric structure of a C-type mannose-binding protein.";
Structure 2:1227-1240(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 124-238.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 124-238.
   238 AA
                                                                                                                                                                                                       SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 262:2582-2589(1987).
                                                                                                                                                                                                                                                                                                                          apoprotein.";
J. Biol. Chem. 261:6878-6887(1986)
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Liver;
MEDLINE=87137502; PubMed=3029088;
                                                                                                                                                                                                                       TISSUE=Liver;
MEDLINE=86196130; PubMed=3009480;
                                 01-FEB-1991 (Rel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                              Drickamer K., McCreary V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 360:127-134(1992).
 STANDARD;
                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 18-42.
                                                                                                                                                                     NCBI_TaxID=10116;
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Complement pathway; Membrane; Mannose-binding; Calcium; Repeat;
Signal; Collagen; Lectin; Glycoprotein; Hydroxylation; 3D-structure.
SIMILARITY: Contains 1 collagenous domain. SIMILARITY: Contains 1 C-type lectin family domain.
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C-TYPE LECTIN (SHORT HYDROXYLATION (POTENT
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InterPro; IPR001304; Lectin_C.
Pfam; PF01391; Collagen; 1.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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Homo sapiens
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94 LysLeuAlaAsnMetGluAlaGluIleAsnThrLeuLysSerLysLeuGluLeuThrAsn 113
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|GluGluThrLeuLysThrCys---SerValIleAlaCys-----
                                                                                      25308 MW; 1A927482B8A8CB3D CRC64;
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Mismatches:
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Matches:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Structure 7:255-264(1999).

C. -!- FUNCTION: Contributes to the lung's defense against inhaled microorganisms. Binds strongly maltose residues and to a lesser extract other alpha-glucosyl moieties. It could participate in the extracellular reorganization or turnover of pulmonary surfactant.

C. -!- SUBGUIT: Oligomeric complex of 4 set of homotrimers.

C. -!- SUBGUIT: Oligomeric complex of 4 set of homotrimers.

C. -!- PTM: The N-terminus is blocked.

C. -!- PTM: The N-terminus is blocked.

C. -!- PTM: There are 4 surfacellular.

C. -!- PTM: There are 4 surfacellular.

C. -- MISCELLANEOUS: Pulmonary surfactant consists of 90% lipid and 10% protein. There are 4 surfacellular (SP-A and SP-D) and 2 small hydrophobic proteins (SP-A and SP-D) and 2 small hydrophobic proteins (SP-B and SP-C).

C. -!- SIMILARITY: Contains 1 collagenous domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Crouch E., Rust K., Veile R., Donis-Keller H., Grosso L., "Genomic organization of human surfactant protein D (SP-D). SP-D is encoded on chromosome 10q22.2-23.1.", J. Biol. Chem. 268:2976-2983(1993).
                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-COT-2003 (Rel. 42, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D) (FSP-D)
SFTPD OR SFTP4 OR PSPD.
                                                                                                                                                                                                                                                                        Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92322003; PubMed=1339284;
Lu J., Willis A.C., Reid K.B.M.;
"Purification, characterization and cDNA cloning of human lung
surfactant protein D.";
Biochem. J. 284:795-802(1992).
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Cai G.-Z., Crouch B.,
"Human surfactant protein D: SP-D contains a C-type lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 60-375 FROM N.A., AND PARTIAL SEQUENCE
375 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carbohydrate recognition domain.";
Arch. Biochem. Biophys. 290:116-126(1991).
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PRT;
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MEDLINE=91378578; PubMed=1898081;
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EMBL; L05484; AAB59450.1; JOINED.
EMBL; X65018; CAA46152.1; -.
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TISSUE=Amniotic fluid, and Lung
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Mammalia; Eutheria; Primates;
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   STANDARD;
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PDB; 1B08; 29-NOV-99.
                                                                                                                                                                                                                                               (Human)
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149 AlaProGlyMetGlnGlySerAlaGlyAlaArgGlyLeuAlaGlyProLysGlyGluArg 168
                                    GGGGAACCAGGCCAA------GGGCTCAGAGGCTTACAGGGCCCCCCTGGAAG 225
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                                                                                                                                                                                                                                    AAAGCT-----CTGCAAAATGGCACGTATC 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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--- SUBCELLULAR LOCATION: Secreted.
--- TISSUE SPECIFICITY: Highly expressed in thymus and liver.
--- PTM: Hydroxylated (Potential).
--- SIMILARITY: Contains 1 collagenous domain.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Collectin-46 precursor (CL-46) (46 kDa collectin)
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D -> P (IN REF. 3)

E -> EH (IN REF. 3)
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                                               LysGlyGluArgGlyAlaProGlyGluLeuGlyAlaProGlySerAlaGlyValAlaGly 178
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GlyAspArgGlyAspProGlyGluArgGlyAlaLysGlyGluSerGlyLeuAlaAspVal
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Lu J., Laursen S.B., Thiel S., Jensenius J.C., Reid B.M.;
"The cDNA cloning of conglutinin and identification of liver as a
primary site of synthesis of conglutinin in members of the Bovidae.";
Biochem. J. 292:157-162(1993).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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conglutinin.";
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01-N0V-1991 (Rel. 20, Created)
01-FEB-1994 (Rel. 28, Last seq
01-OCT-1996 (Rel. 34, Last ann
Conglutinin precursor.
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SEQUENCE FROM N.A.
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                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL; AF509590; AAM34743.1; -.

InterPro; IPRO08160; Collagen.

InterPro; IPRO01304; Lectin C.

Pfam; PF01391; Collagen; 2.

Pfam; PF00034; Lectin C; 1.

SMART; SR00034; CLCTT; 1.

PROSITE; PS50041; C.TYPE LECTIN 1; 1.

PROSITE; PS50041; C.TYPE LECTIN 2; 1.

Lectin; Hydroxylation; Glycoprofein; Mannose-binding; Membrane; Collagen; Repeat; Calcium; Signal.

SIGNAL
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108AC45A91420E83 CRC64;
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BY SIMILARITY.
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C-TYPE LECTIN (SHORT FORM)
SIMILARITY: Contains 1 C-type lectin family domain.
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Mismatches:
Indels:
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Matches:
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Liou L.S., Saetry R., Hartshorn K.L., Lee Y.M., Okarma T.B.,
Tauber A.I., Ssetry K.N.;
Howine conglutinin (BC) mRNA expressed in liver: cloning and
characterization of the BC cDNA reveals strong homology to surfactant
                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Liver;
MEDLINE-94128104; PubMed-8297370;
Kawasaki N., Itoh N., Kawasaki T.;
"Gene organization and 5'-flanking region sequence of conglutinin: a C-type mammalian lectin containing a collagen-like domain.";
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Tauber A.I., Sastry K.N.;
Bovine conglutinin gene exon structure reveals its evolutionary relationship to surfactant protein-D.";
J. Immunol. 153:173-180(1994).
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MEDILINE=91131556, PubMed=1993651;
Lee Y.-M., Leiby K.R., Allar J., Paris K., Lerch B., Okarma T.B.
"Primary structure of bovine conglutinin, a member of the C-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biol. Chem. 266:2715-2723(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY SEQUENCE OF 21-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D14085; BAA03170.1; -. EMBL; X71774; CAA50665.1; -. EMBL; L18871; AAA20126.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U06855; AAB60624.1;
U06856; AAB60624.1;
U06857; AAB60624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D25300; BAA04983.2;
D25301; BAA04983.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U06860; AAB60624.1;
U06854; AAB60624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U06858; AAB60624.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BAA04983.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAA04983.2;
BAA04983.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D25299; BAA04983.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BAA04983.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB60624.1
                                                                                                                                       Gene 141:277-281(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lectin family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D25301; BAA049
145878; 145878.
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D25296;
                                                                                                                                                                                                LISSUE=Semen;
                                                                                                                  protein-D."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
EMBL;
EMBL;
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EMBL;
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EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 AlabrodlyIleGlnGlyPheProGlyPro-----SerGlyLeuLysGlyGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              |||||||||||:::::
203 AspProGlyGluThrGlyAlaLysGlyGluSerGlyLeuAlaGluValAsnAlaLeuLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 LysLysAlaValLeuPheProAspGlyGlnAlaValGlyGluLysIlePheLysThrAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 TCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGGAACCAGGCCAA------GGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       226 TTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 IleGlyProGlnGlyProSerGlyAlaArgGlyProProGlyLeuLysGlyAspArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                367 AAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAAT
R HSSP; P35247; LB08.
R InterPro; IPR008161; C1g helix.
R InterPro; IPR008161; C21g helix.
R InterPro; IPR008161; C21g helix.
R Pfam; PF01391; C01lagen; 3.
R Pfam; PF00059; lectin c; 1.
R ProDom; PD000007; C1g_helix; 1.
R PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
R PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
R PROSITE; PS044; C_TYPE_LECTIN_2; 1.
R Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Membrane; S1CSNAL.
S1CSNAL.
T S1CSNAL.
                                                                                                                                                                                                                                                                                                                             HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
CELL ATTACHMENT SITE (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLORAC. ..) (POTENTIAL).
K -> H (IN REF. 2 AND 3).
K -> S (IN REF. 6).
K -> A (IN REF. 5).
E -> V (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACCCTGGAAAAGT - - - CCGGATGGTGATAGTAGCCTGGCTGCC - - - -
                                                                                                                                                                                                                                           (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         867BB41992544B1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
91
39
74
25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative:
Mismatches:
                                                                                                                                                                                                                       COLLAGEN-LIKE.
C-TYPE LECTIN (HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
                                                                                                                                                                                                                                                                                                  HYDROXYLATION
HYDROXYLATION
                                                                                                                                                                                                                                                                      HYDROXYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37994 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.41e-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   441.50
56.77%
39.74%
32.34%
                                                                                                                                                                                                                                                                   371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                         21
46
273
63
87
87
87
135
141
159
162
162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   286
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328
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                                                                                                                                                                                                                                       DOMAIN
MOD_RES
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SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
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                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . No. :
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70 ACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCTCCAGGCATC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84 GlyProLysGlyGluAsnGlySerAlaGlyGluProGlyProLysGlyGluArgGlyLeu 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 ValGlyProProGlySerProGlyIleSerGlyProAlaGlyLysGluGlyProSerGly 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF0131; Collagen; 3.
Pfam; PF0059; lectin_c; 1.
PROSITE; SM00054; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation; Signal; Lectin; Collagen; Repeat; Coiled coil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCAGAAACTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24 ThrLeuSerGlnArgSerIleThrAsnThrCysThrLeuValLeuCysSerProThrGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 0 AACGGCTTCCCAGGCAAAGATGGGCGTGAT-----GGCACCAAGGGAAAAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 AspProGlyLeuProGlyProMetGlyLeuSerGlyLeuProGlyProArgGlyProVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----CAAGGGCTCAGAGGCTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144 GlyGluValGlyAlaProGlyMetGlnGlySerAlaGlyAlaLysGlyProAlaGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAAGTCCGGATGGT---
                                                                                                                                                                                                                                           PULMONARY SURFACTANT-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                     C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
N-LIRKED (GLCNAC. . .).
HYDROXYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYDROXYLATION.

N -> E (IN REF. 2).

K -> C (IN REF. 2).

DB2BB5E399DB4A3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    374
1110
34
99
128
                                                                                                                                                                                                                                                                                                        COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROXYLATION. HYDROXYLATION.
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HYDROXYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-054-536-2 (1-747) x PSPD RAT (1-374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGCCAAAAAGGAGACCCTGGA
                                    InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37561 MW.
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38.81%
29.65%
32.31%
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2253
3374
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777
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176
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176
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                   P35247; 1B08.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 GAACCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity:
                                                                                                                                                                                                    Signal; Lectin;
SIGNAL 1
CHAIN 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                       DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                     MOD RES
MOD RES
MOD RES
MOD RES
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               343 GlnProGluAsnCysValGluIlePheProAspGlyLysTrpAsnAspValProCysSer 362
                                                                                597
                                                                                                                                                              651
                                                                                                                                                                                                                                             711
537
                       303 LysAsnAlaTyrLeuSerMetAsnAspIleSerThrGluGlyArgPheThrTyrProThr
                                                                                GAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACA
                                                                                                                                                              GGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCT-----GGT
                                                                                                                                                                                                                                             652 TCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      surfactant protein D. cDNA and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (PSP-D)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIINE=90001186; PubMed=2675969;
Persson A., Chang D., Rust K., Moxley M., Longmore W., Crouch
"Purification and biochemical characterization of CP4 (SP-D),
GCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimizu H., Fisher J.H., Papst P., Benson B.,
Voelker D.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    374 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 20-33.
TISSUE=Lung;
                                                                                                                                                                                                                                                                                                                           712 ACCICCCATCIGGCCGICTGIGAGIIC 738
                                                                                                                                                                                                                                                                                                                                                     LysGlnLeuLeuVallleCysGluPhe 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Primary structure of rat pulmonary deduced amino acid sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 267:1853-1857(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=92112913; PubMed=1370483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 73-95 AND 153-180.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M81231; AAA42170.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, 01-FEB-1994 (Rel. 28, 15-JUL-1999 (Rel. 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia, Eutheri
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SFTPD OR SFTP4
                                                                                                                                                                                                                                                                                                                                                                   363
                                        283
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REBL; BC003/us; .....

RESP; P35247; 1B08.

RESP; P35247; 1B08.

DR MGD; MG1109515; SEFPG.

DR MGD; MG1109515; SEFPG.

DR InterPro; IPR001304; Lectin_C.

DR Pfam; PF00059; lectin_c; 1.

DR PR001TE; PS00615; C_TYPE_LECTIN_1; 1.

DR PR05ITE; PS00615; C_TYPE_LECTIN_2; 1.

RW Glycoprotein; Calcium; Surface film; Gaseous exchange, Hydroxylation; KW Glycoprotein; Collagen; Repeat; Coiled coil.

KW Signal; Lectin, Collagen; Repeat; Coiled coil.

The Collagen; Repeat; Coiled coil.

ATA PULMONARY SURFACTANT-ASSOCIATED PROTEIN
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                                                                                                                                                      MEDLINE-2138257; PubMed=12477932;

MEDLINE-2138257; PubMed=12477932;

MEDLINE-2138257; PubMed=12477932;

MEDLINE-2138257; PubMed=12477932;

MA Strausberg R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

MA Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A Diatchenko L., Marusina K., Parmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gubarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mitching M., Madan A., Young A.C., Schwuct S.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butkeelield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Mannerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Mannerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Mannerfield Y.S.N., Krzywinski M.I., Marra M.A.,

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COLLED COIL (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
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AF047741, AAD31380.1; JOINED.
AF192134; AAF1277.1; -.
BC003705; AAH03705.1; -.
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EMBL; AF047742; AAD31380
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HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 PheSerArgTyrLysLysBlaAlaLeuPheProAspGlyGlnSerValGlyAspLysIle
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264 PheArgAlaAlaAsnSerGluGluProPheGluAspAlaLysGluMetCysArgGlnAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 GlyGlyGlnLeuAlaSerProArgSerAlaThrGluAsnAlaAlaValGlnGlnLeuVal
                                                                                                                                                                                                                                                 204 GlyAspArgGlyAlaProGlyAspArgGlyIleLysGlyGluSerGlyLeuProAspSer
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                                                                                                                                        184 ProAlaGlyProAlaGlyProGlnGlyAlaProGlySerArgGlyProProGlyLeuLys
                                                                                                                                                                                              -----GATAGT
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Lawson P.R., Perkins V.C., Holmskov U., Reid K.B.;
"Genomic organization of the mouse gene for lung surfactant protein
                                                                                                                                                                                                                                                                                                       AGCCTGGCTGCCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCACGTATC-----
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01-077-1996 (Rel. 34, Last sequence update)
10-077-2003 (Rel. 42, Last annotation update)
10-077-2003 (Rel. 42, Last annotation update)
Pulmonary surfactant-associated protein D precursor (SP-D) (PSP-D)
SFTPD OR SFTP4
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musnae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Respir. Cell Mol. Biol. 20:953-963(1999).
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FT CARBOHYD 89 89 N-LINKED (GLCNAC) (POTENTIAL).  SQ SEQUENCE 374 AA; 37688 MW; FE034261263F43E4 CRC64;  Alignment Scores:	THICKARTACTCCCTTCTCTCGATATATGGTG.  SUPTOPHELEUSERMETLEUVALLEUVALGINPrOLEUGIJASNILEU  SUGAAACTGTGACCTGTGAGGATGCCCAAAAGAGGGGTGATT  STELYSSETLEUSERGINARGSETVAIPTOASNTHICYSTHILEUVALMELU  STELYSSETLEUSERGINARGSETVAIPTOASNTHICYSTHILEUVALMELU  STELYSSETLEUSERGINARGSETVAIPTOASNTHICYSTHILEUVALMELU  STELYSSETLEUSERGINARGSETVAIPTOASNTHICYSTHILEUVALMELU  STELYSSETLEUSERGINARGSETVAIPTOASNTHICYSTHILEUVALMELU  STELYSSETLEUSERGINARGGGCAACCAGC  STELYSSETLEUSERGINARGGGCAACCAGC  STELYSSETLEUSERGINARGGGCAGCAGCAGC  STELYSSETLEUSERGINARGGGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC	239 ArgLeuGluValAlaPheSerHisTyrGlnLysAlaAlaLeuPhProAspGlyArgSer 258 400 GTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCC 459        :::
FT CARBG SQ SEQUI Alignment Pred. No. Score: Percent S. Best Local Query Mate DB:	6	8 6 8 6 B

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tute of Bioinformatics and the EMBL outstation-ics Institute. There are no restrictions on its fitutions as long as its content is in no way ent is not removed. Usage by and for commercial nse agreement (See http://www.isb-sib.ch/announce/nse@isb-sib.ch).
------AAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAG 570 ::: ||||||| :::||||||| hralaHisAsnLysAlaAlaPheLeuSerMetThrAspValGly 318
                                                                                                                                                                                                                        ||| ||||||||| :::||||||| :::
|snGlyGlyAlaGluAsnCysValGluIlePheThrAsnGlyGln 358
                                                                                                TGGATCTGACAGGAAATAGACTGACCTACACAAACTGGAACGAG 630
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hrTyrProThrGluProLeuValTyrSerAsnTrpAlaPro 338
                                                                                                                                                                                             CTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAATGGCCAG 690
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bovine collectin-43 (CL-43). Comparison with unfactent protein-D.";

220-11824(1994).

520-11824(1994).

510-11824 and sugars: mannose = manNAc > glucose = maltose > glactose > lactose > lactose > (a complex of 4 set of homotrimers.)

ic complex of 4 set of homotrimers.

[Y: Liver specific.

[Potential]
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ler V., Vitved L., Bendixen C., Skjoedt K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lata; Craniata; Vertebrata; Euteleostomi;
tiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                naracterization of CL-43 and its proximal
                                                                                                                                                                                                                                                                                        738
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Reid K.B.M., Lu J., Laursen S.B.,
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1 C-type lectin family domain.
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st annotation update)
CL-43) (43 kDa collectin).
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EMBL; J03542; AAA31465.1; -. EMBL; L19387; AAA31468.1; -.
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|GluThrSerValLeuGluValAspThrLeuArgGlnArgMetArgAsnLeuGluGlyGlu
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                                                                                                                                                                                                                                                                                               41 AlaProProAlaAspSerLeuArgGlyHisAspGlyArgAspGlyLysGluGlyProGln
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                                                                                                                                                                                                                           --TGCCCTGCAGTGATTGCCTGT
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                                                                                                                                                                                                                                                                                                                 ------CAAGGCTCAGAGGCTTACAGGGCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 AGAAAAGCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTGACCTTCTCTCTGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 AAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAGTG
Pfam; PF00059; lectin_c; 1.
SMARY; SM0034; CLECT; 1.
PROSITE; PS00015; C_TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Hydroxylation; Glycoprotein; Mannose-binding; Collagen; Stepat; Calcin; signal.
1 20
                                                       COLLECTIN-43.
CCLLAGEN-LIKE.
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
BY SIMILARITY.
T -> A (IN REF. 2).
N -> A (IN REF. 2).
W, 12BF120BB48861A1 CRC64;
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Matches:
Conservative:
Mismatches:
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Mendelson C.R.;

"Rabbit lung surfactant protein A gene: identification of a lung-
specific Danse I Hypersensitive site.";

The physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

"In Physiol. 262:L662-L671(1922).

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                                                                      676 CTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTGAG
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-GAGGAAGCCTTCCTGGGCATCACTGAT
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Boggaram V., Qing K., Mendelson C.R.;
The major apoprotein of rabbit pulmonary surfactant. Elucidation of rary sequence and cyclic AMP and developmental regulation.";
J. Biol. Chem. 263:2939-2947(1988).
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
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01-0CT-1989 (Rel. 12, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
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GGAGCCATTCAGAATCTCATCAAG---
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SFTPA1 OR SFTPA OR SFTP1.
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IleValLysGluArgAsnThrTyrAlaTyrLeuGlyLeuAlaGluGlyProThrAlaGly 195
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                                                                                                                                                                                                                                                                                                                                                                                                                      44 AspGlyArgAspGlyValLysGlyAspProGlyProProGlyProMetGlyProProGly
                                  Pfam; PF01391; Collagen; 2.
Pfam; PF00159; lectin c; 1.
SMART; SMO0034; CLECT; 1.
PROSTIE; PS00615; C TYPE LECTIN 1; 1.
PROSTIE; PS50041; C TYPE LECTIN 2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation;
                                                                                             Signal, Lectin, Collagen, Repeat.
SIGNAL 1 15 POTENTIAL.
CHAIN 16 247 PULMONARY SURFACTANT-ASSOCIATED PROTEIN
                                                                                                                                                                        . .) (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                    148 GATGGGCGTGATGGCACCAAGGGAAAAGGGGGAACCAGGCCAA----
                                                                                                                        A. COLLAGEN-LIKE.
COLLAGEN-LIKE.
BY SIMILARITY.
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N-LINKED (GLCNAC. . .) (PROB S -> APWA (IN REF. 2).
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289634054CBC8CB4 CRC64;
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Matches:
Conservative:
Mismatches:
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237 B
206 N-
12 S
60 GF
26071 MW;
       HSSP, P22897; 1EGG.
InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin_C.
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417.50
52.17%
35.97%
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                                                                                                                                      669
                                                                                                                                                                                                       234
639
                                                         196 AspPheTyrTyrLeuAspGlyAspProValAsnTyrThrAsnTrpTyrProGlyGluPro 215
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InterPro; IRRO01304; Lectin_C.
Pfam; PP01391; Collagen; 2.
Pfam; PP01391; Collagen; 2.
Pfam; PF0059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Calcium; Surface film; Gaseous exchange; Hydroxylation; Signal; Lectin; Collagen; Repeat; Coiled coil.
Signal; 1.

369 PULMONARY SURFACTANT-ASSOCIATED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunology 78:159-165(1933).

-!- FUNCTION: Contributes to the lung's defense against inhaled microorganisms. Binds strongly maltose residues and to a lesser extent other alpha-glucosyl moieties. It could participate in the extracellular reorganization or turnover of pulmonary surfactant.

-!- SUBGNIT: Oligomeric complex of 4 set of homotrimers.

-!- SUBCELLULANEOUS: Pulmonary surfactant consists of 90% lipid and 10% protein. There are 4 surfactant associated protein: 2 collagenous, carbohydrate-binding glycoproteins (SP-A and SP-D) and 2 small hydrophobic proteins (SP-B and SP-C).

-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                 640 AACAATGCTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGAC
580 CAGTITGIGGAICTGACAGGAAATAGACTGACCTACACAAACTGGAACGAGGTGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bos taurus (Bovine).
Wakaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinee; Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lim B.L., Lu J., Reid K.B.M.; Structural similarity between bovine conglutinin and bovine lung surfactant protein D and demonstration of liver as a site of synthesis of conglutinin.";
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COILED COIL (POTENTIAL).
C-TYPE LECTIN (SHORT FORM).
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
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MEDLINE=93170856; PubMed=8436402;
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US-10-054-536-2 (1-747) x PSPA_CAVPO (1-247)
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SCUENCE FROM N.A.

SECURICE FROM N.A.

SECURICE FROM N.A.

STRAIN=Hartley; TISSUE=Lung;

X MEDLINE=9018900; bubMed=9157868;

XMEDLINE=9018900; bubMed=9157868;

XA Vann H.T., Gowan S., Kelly F.J., Bingle C.D.;

RT "Cloning of guinea pig surfactant protein A defines a distinct
RT cellular distribution pattern within the lung.";

RT Am. J. Physiol. 273:L900-L906(1997).

-I- FUNCTION: In presence of calcium ions, PSAP binds to surfactant phospholipids and contributes to lower the surface tension at the cair—liquid interface in the alveoli of the mammalian lung and is essential for normal respiration.

-I- SUBMITT: Oligomeric complex of 6 set of homotrimers.

CC -I- SUBCELLULAR LOCATION: Extracellular.

CC -I- MISCELLARROUS: Pulmonary surfactant consists of 90% lipid and 10% protein. There are 4 surfactant associated protein: 2 collagenous, CC carbohydrate-binding Glycoproteins (SP-A and SP-D) and 2 small hydrophobic proteins (SP-B and SP-C).

CC -I- SIMILARITY: Contains 1 collagenous domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                              (SP-A) (PSP-A)
                                                                                                                                                                                      Cavia porcellus (Guinea pig).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Hystricognathi; Caviidae; Cavia.
NCBI TaxID=10141;
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COLLAGEN-LIKE.
C-TYPE LECTIN (SHORT FORM).
BY SIMILARITY.
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N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pulmonary surfactant-associated protein A precursor
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Mismatches:
Indels:
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HSSP; P22897; IEGG.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Collagen.
InterPro; IPR001304; Lectin.C.
Pfam; PF001931; Collagen; 1.
Pfam; PF00199; Iccin.C.; 1.
Probom; PD0000007; Clg helix; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS0041; CLECT; 1.
PROSITE; PS0041; CTYPE LECTIN 1; 1.
PROSITE; PS0041; CTYPE LECTIN 2; 1.
Glycoprotein; Calcium; Surface Film; Gaseous exc Signal; Lectin; Collagen; Repeater.
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y 16 TCACTCCCTCTCTCTGAGTAIGGCGCGCGTCTTACTCAGAAACTGTGACCTGT 75	y 76 GAGGATGCCCAAAAGACCTGCCTGCAGTGATTGCCTGTAGCTCTCCAGGCATCAACGGC 135	y 136 TTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAGGGGGAACCAGGCCAAGGG 195	y 196 CTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCT 255	y 256GGGTCACCAGGACCAAAAGGGCCAAAAAGGACCCTGGAAAA 297 	y 298 AGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAA	y 358 GCACGTATCAAAAG399 :::	y 400GTTGGGAACAAGTTCTTCCTGACCAATGGTGAAATAATGACCTTTGAAAAGTG 453	y 454 AAGGCCTTGTGTGTAGTTCCAGGCCTCTGTGCCACCCCCAGGAATGCTGCAGAAT513	y 514 GGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTTCCTGGGCATCACTGAT 564         :::::::   ::: b 171 ThralalleSerSerlleValLySLysTyrAsnIleTyrSerTyrLeuGlyLeuThrGlu 190	y 565 GAGAAGACAGAAGAGGGAGTTTGTGGGTCTGGCAAGAAATAGACTGACCTACACAAAACTGG 624  191 GlyHisThrProGlyAspPheHisTyrLeuAspGlySerProLeuAsnTyrThrAsnTrp 210	OY 625 AACGAGGGGAGAACCCAACAATGCTGGATGAAGATTGTGTATTGCTACTGAAAAAT 684	OY 685 GGCCAGTGGAATGACGTCCCTGCTCCCATCTGGGCGTCTGTGAGTTC 738	
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Search completed: June 18, 2004, 21:00:53 Job time : 20 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nuc	nnoleic search, nsing aw model
on:	21, 2004, 16:39:3
Title: Perfect score: Sequence:	US-10-054-536-2 747 1 atgtccctgtttccatcacttctgtgagttccctatctga 747
Scoring table:	IDENTITY_NUC Gapop 10.0 , Gapext 1.0
Searched:	3470272 seqs, 21671516995 residues
Total number of	hits satisfying chosen parameters: 6940544
Minimum DB seg Maximum DB seg	length: 0 length: 2000000000
Post-processing	: Minimum Match 0% Maximum Match 100% Listing first 45 summaries
Database :	GenEmbl:*  11 9b ba:*  21 9b ha:*  41 9b ba:*  42 9b hi:*  43 9b in:*  43 9b in:*  44 9b on:*  45 9b on:*  46 9b on:*  47 9b ph:*  48 9b ph:*  49 9b ph:*  40 0 m:*  40 0 m:*  41 9b pa:*  41 9b pa:*  42 9b ph:*  43 9b ph:*  44 9b ph:*  45 9b ph:*  46 0 m:*  47 9b ph:*  48 9b ph:*  49 9b ph:*  40 0 mus:*  41 9b pa:*  41 9b pa:*  42 9b ph:*  43 9b ph:*  44 9b ph:*  45 9b ph:*  46 9b ph:*  47 9b ph:*  48 9b ph:*  48 9b ph:*  49 9b ph:*  40 9b ph:*  41 9b ph:*  42 9b ph:*  43 9b ph:*  44 9b ph:*  45 9b ph:*  46 9b ph:*  47 9b ph:*  48 9b ph:*  4

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Length	DB	ID	Description
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е	747	8	1632		HOSA16576	Homo
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9	747	8	1638		HOSA16581	16581 Homo
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σ	747	00	3605		HSMBPC	Humar
10	745.4	σ	1632		HOSA16578	Y16578 Homo sapien
11	10	σ	1638		HOSA16579	Homo
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14	10	S	1188		109220	
15	7	œ	805		MACMBPC	L43911 Macaca mula
16	₹#	თ	1409		D73408	D73408 Bos taurus
17	LO	⋖	723		AF164576	-
18	~	N	1010		E37364	E37364 Swine serum
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## ALIGNMENTS

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ם ייי	159/79	Recombinant	the same.	E27637	E27637.1 GI:13018239	JP 1999206378-A/2.	unidentified	unidentified	unclassified.	1 (bases 1 to 747)	Nobutaka, W.	Recombinant	the same
RESULT 1 E27637	LOCUS	DEFINITION		ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM		REFERENCE	AUTHORS	TITLE	

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                                                                                                                AR182149 900 bp
Sequence 1 from patent US 6337193.
AR182149
                              CTGGCCGTCTGTGAGTTCCCTATCTGA 747
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C12N15/09,COXK44/17,C12P21/02//A61K38/00,(C12N15/09,C12R1:91),
(C12P21/02,C12R1:91),C12N15/00,A61K37/02,(C12N15/00,C12R1:91)
Strandedness: Double;
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                                                                                                                                                                                                /organism='Unidentified'
Location/Qualifiers
1. .747
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/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                   100.0%; Score 747; DB 6; I 100.0%; Pred. No. 2.3e-209;
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 03-AUG-1999;
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                           Unidentified
JP 1999206378-A/2
03-AUG-1999
23-JAN-1998 JP 1998011864
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Patent: JP 1999206378-A
FUSO YAKUHIN KOGYO KK
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/product="mannose-binding lectin"
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Homo sapiens gene encoding mannan/mannose-binding protein, variant
                                     Madsen, H.O.
Direct Submission
Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
Immunology, Section 7631, National University Hospital, Tagensvej
20, DX-2200 Copenhagen, DENMARK
Related sequences X15954, X15955, X15956, X15422.
Location/Qualifiers
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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note="polymorphism in different MBL haplotypes"
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'note="MBL haplotype LYQA"
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/db xref="taxon:9606"
/chromosome="10"
                                                                                                                                                                       CTGGCCGTCTGTGAGTTCCCTATCTGA 812
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100.0%; Pred. No. 2.5e-209;
iive 0; Mismatches 0;
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Best Local Similarity
Matches 747; Conserv
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1546 GATTGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 1605
                                                                                                                                                                                                                         PRI 17-SEP-1999
                                                                                                                                                                                                                                             Homo sapiens gene encoding mannan/mannose-binding protein, variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical
Immunology, Section 7631, National University Hospital, Tagensvej
20, DK-2200 Copenhagen, DENWARK
Related sequences X15954, X15955, X15956, X15422.
                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata, Vertebrata, Euteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Madsen, H.O., Satz, M.L., Hogh, B., Svejgaard, A. and Garred, P. Different molecular events result in low protein levels of mannan-binding lectin in populations from southeast Africa and
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495. .500
/note="polymorphism in different MBL haplotypes"
745. .1638
/gene="MBL"
745. .750
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86. .791
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/product=mannose-binding lectin"
/protein_id="CAB56120.1"
/db_xref="G1:5911792"
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    1638
    organism="Homo sapiens"

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/db_xref="taxon:9606"
/chromosome="10"
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Primates;
                                                721 CIGGCCGTCIGIGAGIICCCIAICIGA
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mannose-binding lectin; mbl
Homo sapiens (human)
Homo sapiens
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/gene="MBL"
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/gene="MBL"
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Mammalia; Eutheria;
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Direct Submission
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SVATPKNAABRIKALQNILKERAFLGITDEKTEGQFVDLTGNKLTYTNWNEGEPNNAGS
DEDCVLLLKNGQWNDVPCSTSHLAVCEFPI"
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/note="polymorphism in different MBL haplotypes"
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                                                                                                             HOSA16580 1638 bp DNA linear PRI 17-SEP-1999
Homo sapiens gene encoding mannan/mannose-binding protein, variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical Immunology, Section 7631, National University Hospital, Tagensvej 20, DK-220G Copenhagen, DENMARK Related sequences XIS954, XIS955, XIS956, XI5422. Location/Qualifiers
                                                                                                                                                                                                                                                        Craniata, Vertebrata, Buteleostomi,
Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                           Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P. Different molecular events result in low protein levels of mannan-binding lectin in populations from southeast Africa
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mannose-binding lectin; mbl gene.
Homo sapiens (human)
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100.0%; Pred. No. 2.5e-209;
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Homo sapiens gene encoding mannan/mannose-binding protein, variant
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical Immunology, Section 7631, National University Hospital, Tagensvej 20, DK-2200 Copenhagen, DENMARK Related sequences X15554, X15955, X15956, X15422.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/db_xref="GOA:P11226"
/db_xref="SWISS-PROT:P11226"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                       546 TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG
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AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA
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Best Local Similarity 100.0%; Pred. No. 2.8e-209;
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Recombinant human mannan binding protein and process for producing
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                                                                                                                                                                                                                                                                               Recombinant human mannan binding protein and process for producing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCA 360
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                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3605)
Nobutaka,W.
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Pred. No. 2.8e-209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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100.0%; Pred. No. z...
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide 66. .125
66. .812.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            23-JAN-1998 JP 1998011864
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FUSO YAKUHIN KOGYO KK
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JP 1999206378-A/1
03-AUG-1999
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                                                                                                                                            GI:13018238
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JP 1999206378-A/1.
Homo sapiens (human)
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KEYWORDS
SOURCE
ORGANISM
                                                                                      DEFINITION
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TITLE
                                                                                                                       ACCESSION
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Gaps

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SVATPRNAAENGAIQNLIKEBAFIGTTDEKTEGGFVDLTGNRLTYTNWNBGSPNNAGS
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/product="mat. mannose-binding protein C (AA 1-228)
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/note="signal peptide (AA -20 to
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The human mannose-binding protein gene. Exon structure reveals its evolutionary relationship to a human pulmonary surfactant gene and localization to chromosome 10 90010778

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Bzekowitz,R.A.B.
Direct Submission
Submitted (17-AUG-1989) Bzekowitz R.A.B., The Children's Hospital,
Enders Building 7th Floor, 300 Longwood Avenue, Boston MA 02115, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 3605)
Sastry, K., Herman, G.A., Day, L., Deignan, E., Bruns, G., Morton, C.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S.A. X15422 revises MBP cDNA seq published by:
Ezekowitz et. al. J. Exp. Med. 167;1034-1046(1988). Data kindly reviewed (22-FEB-1990) by Ezckowitz R.A.B.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                    GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGCAGTTTGTGGATCTGACAGGA
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                                                         CGTATCAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCT
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X15422
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| mol Lype="mRNA"
| db xref="taxon:9606"
| chromosome="10q11.2-q21."
| clone="48-11"
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66. .812
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/note="polymorphism in different MBL haplotypes"
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/note="polymorphism in different MBL haplotypes"
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Pred. No. 7.5e-209;
0; Mismatches 1;
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       /gene="MBL"
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Best Local Similarity 99.9%;
Matches 746; Conservative
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GPPGPKGNCPGTYKERKGPPGGLIGGLGPPGKLGSPPGNDEDSGSPGPKGCKGDPCKSPD
GDSSLAASBEKALOFFBAR IKWLTFSLGKOYGNKFPLTNGELMTFEKVKALOKFQA
SVATPRNAASHGAIONLIKEEAFLGITDEKTEGGFVDLTGNRLTYTNWNEGEPNNAGS
                                                      PRI 17-SEP-1999
                                                  HOSA16578 17-SEP-199 HOM linear PRI 17-SEP-199 Homo sapiens gene encoding mannan/mannose-binding protein, variant
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-FBB-1998) H.O. Madsen, Department of Clinical
Immunology, Section 7631, National University Hospital, Tagensvej
20, DK-2200 Copenhagen, DENMARK
Related sequences X15954, X15955, X15956, X15422.
Location/Qualifiers
                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                    Madsen, H.O., Satz, M.L., Hogh, B., Svejgaard, A. and Garred, P. Different molecular events result in low protein levels of mannan-binding lectin in populations from southeast Africa
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/protein.id="CAB56045.1"
/db_xref="GI:5911794"
/db_xref="GOA:P11226"
/db_xref="GOA:P11226"
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/db xref="taxon:9606"
/chromosome="10"
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HOSA16582 1638 bp DNA linear PRI 17-SEP-1999
Homo sapiens gene encoding mannan/mannose-binding protein, variant
HYPD.
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                                                      /gene="MBL"
/note="polymorphism in different MBL haplotypes"
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                                                                                                                                                                                                                  Length 1638;
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                                                                                                                                                                                                                    Score 745.4; DB 9;
Pred. No. 7.5e-209;
0; Mismatches 1;
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SVATPRNAAABKGAIQMINIKEBAFLGTIDEKTEGGFVDLTGNRLTYTNWNEGEPNNAGS
PRI 17-SEP-1999
HOSA16579 1638 bp DNA linear PRI 17-SEP-1999
Homo sapiens gene encoding mannan/mannose-binding protein, variant
                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (16-FBB-1998) H.O. Madsen, Department of Clinical
Immunology, Section 7631, National University Hospital, Tagensvej
20, MSK-2200 Copenhagen, DENWARK
Related sequences X15954, X15955, X15956, X15422.
Location/Qualifiers
                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                    Madsen,H.O., Satz,M.L., Hogh,B., Svejgaard,A. and Garred,P. Different molecular events result in low protein levels of mannan-binding lectin in populations from southeast Africa and South America
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'note="polymorphism in different MBL haplotypes"
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Homo sapiens mannan-binding lectin MBL precursor (MBL) mRNA, complete cds.
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                 note="polymorphism in different MBL haplotypes"
                                                                       note="polymorphism in different MBL haplotypes"
                                                                                                         /gene="MBL"
/note="polymorphism in different MBL haplotypes"
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                                                                                                                                                                                 Length 1638;
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                                                                                                                                                                                   Score 745.4; DB 9;
Pred. No. 7.5e-209;
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SVATPRNAAENGAIQNLIKEEAFLGITDEKTEGQFVDLTGNRLTYTNWNEGEPNNAGS
                                                                                                                                                                                                                                                                                                                               Submitted (16-FEB-1998) H.O. Madsen, Department of Clinical Immunology, Section 7631, National University Hospital, Tagensvej 20, DK-2200 Copenhagen, DENMARK Kelated sequences XIS954, XIS955, XIS956, XI5422.

Location/Qualifiers
                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                            Madsen, H.O., Satz, M.L., Hogh, B., Svejgaard, A. and Garred, P. Different molecular events result in low protein levels of mannan-binding lectin in populations from southeast Africa and
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                                                                                                                                                                                                                   Immunol. 161 (6), 3169-3175 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note="MBL haplotype HYPD"
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/db_xref="taxon:9606"
Y16582
Y16582.1 GI:5911808
mannose-binding lectin; mbl gene.
Homo aapiens (human)
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'gene="MBL"
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181 GAACCAGGCCAAGGGCTCAGAGGCCTTACAGGGCCCCCTGGAAAGTTGGGGCCTCC	177 CGIATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 436   421 ACCAATGGTGAAATAATGACCTTTGAAAAAGTGGCCTTGTGTGTG	0y         601         AATAGACTGACCTACACAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA         660           1	RESULT 14   109220	irce 11188 /organism="unknown" /mol_type="unassigned DNA"	Query Match         85.1%;         Score 635.8;         DB 6;         Length 1188;           Best Local Similarity         95.7%;         Pred. No. 1.8e-176;         Added:         Added:         Added:         Added:         Added:         Added:         Bit Index         Bit
VERSION KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Chen, Z., Zhu, X. and Xie, P. Cloning and sequencing of mannan-binding lectin cDNA of Chinese JOURNAL Minyixue Zazhi 15, 83-86 (1999) REFERENCE Chen, Z., Zhu, X. and Xie, P. TITLE Direct Submission JOURNAL Submitted (13-MAR-2001) Immunology, First Military Medical	FEATURES University, 'Jongae, Guangahou, Guangdong 510515, P.K. of China source   1.76	/gene="main-right" / gene="main-right" / codon_start=1 / codon_start=1 / produc="main-nainding lectin MBL precursor" / protein id="AAM52907.1" / db_xref="GI:14030460".1" / db_xref="GI:14030460".1" / db_xref="GI:14030460".1" / cdb_xref="GI:14030460".1" / db_xref="MGI:14030460".1" / dc_me="MGI:14030460".1" / de_me="MGI:14030460".1" / de_me="MGI:14030460".1" / de_me="MGI:14030460".1" / de_me:14030460".1" / de_me="MGI:14030460".1" / de_me="MGI:	variation /gene="MBL"  variation /gene="MBL"  /gene="MBL" /gene="MBL" /note="compared to Homo sapiens mannan-binding lectin encoded by GenBank Accession Number X15422; Ala to Thr substitution" /replace="A"  variation /gene="MBL" /replace="A" /gene="MBL" /replace="A" /replace="A" /gene="MBL" /replace="A" /gene="MBL" /replace="A" /gene="MBL" /replace="A" /gene="MBL" /replace="A" /gene="MBL" /replace="C" /replace="C" /replace="C" /replace="C"	Query Mat Best Loca Matches	Oy         1 ATGCCCGGTTCCATCATCCTTCTCTGAGTAGGGGGTTTACTCA 60           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII

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Mogues, T., Ota, T., Tauber, A.I. and Sastry, K.N.
Characterization of two mannose-binding protein cDNAs from rhesus monkey (Macaca mulatta): structure and evolutionary implications Glycobiology 6 (5), 543-550 (1996)
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               AAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGC
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/organism="Macaca mulatta"
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Macaca mulatta mannose-binding pr
L43911
L43911 GI:1449043
mannose-binding protein.
Macaca mulatta (rhesus monkey)
Macaca mulatta (rhesus monkey)
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Mammalia; Eutheria; Primates; Cat
Cercopitherine; Macaca.
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/sex="male"
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<1. .713
/codon_start=3
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LQTEMARIKKWLTFSLGRQVGNKFFITNGEWTFDKVKALCARFQASVATPRNAAENR
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Pred. No. 2.7e-162;
0; Mismatches 42;
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93.6%;
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Rat lung Bovine co Rat MBP p Rat PrMBP

Antioxida Rat Prote

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Human lun

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Sequence Human 32K

Sequence

Human alv Human NOV

Human 32K Human 32K Human 32K

Minimum DB Maximum DB

Searched:

Sequence:

Run on:

35kd pulm

Plasmid g Genomic

Vector PS Product o

35kd pulm Lung canc

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Human, mannan-binding protein, hMBP, recombinant, inhibition, infection, rhMBP, haemagglutination, influenza, HIV.
Abr42241

Aay77990

Aay77990

Abau764721

Abau36721

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/label= signal
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/label= mannan-binding_protein
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   Command line parameters:
-MODEL=frame+ n2p.model -DEV=xlp
-Q=/Cogn2 1/USPTO spool p/USIN054536/runat 18062004 173454 13562/app query.fasta_1.903
-Q=/Cogn2 1/USPTO spool p/USIN054536/runat 18062004 173454 13562/app query.fasta_1.903
-Q=/Cogn2 1/USPTO spool p/USIN054536/runat SURFIX=rag -MINMATCH=0.1 -LOOPCI_c0
-LOOPEXT=0 -ONITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE_LOCAL -OUTFWT=pto -NORM=ext -HAAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=LOSAL -OUTFWT=pto -NORM=ext -HAAPSIZE=500 -MINLEN=0 -MAXLEN=20000000000
-USER=USIN054336 @CGN 1 181 @runat 18062004 173454 13562 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
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Aab56578 Human man
Aau75574 Human man
Ade87458 248 amino
Aar45005 Human Man
Aay03769 Mannan-bi
Aay03769 Mannan-bi
Aab19401 Pig serum
Aab15401 Pig serum
Aam79745 Human pro
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7471.256 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                 frame_plus_n2p model
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Maximum Match 100%
Listing first 45 summaries
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GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGGCATCAACGCCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
                                                                                                                                 The present invention describes recombinant human mannan-binding protein (rhMBP) having a molecular weight range of 1000-1300 or 200-400 kDa (by gel filtration with detection at 280 nm). rhMBP may be used as a component of drug compositions for the inhibition of haemagglutination and prevention of infection by viruses such as influenza and HIV. The present sequence represents hMBP (human mannan-binding protein)
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                                             Recombinant human mannan-binding protein expressed using pNOW1 vector.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GluThrValThrCysGluAspAlaGlnLysThrCysProAlaValIleAlaCysSerSer
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                      Page 86-87; 91pp; Japanese.
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N-PSDB; AAZ07142, AAZ07143
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Best Local Similarity:
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                                                                                        Disclosure;
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The present invention describes a method (I) for the production of a human recombinant mannan binding lectin (rMBL) composition (C) having size distribution profile at least 50% identical to wild type MBL. The method involves preparing a gene expression construct (EC) encoding MBL or its functional equivalent, transforming a host cell culture (HC) with EC, cultivating HC, subjecting the culture medium to affinity chromatography and obtaining eluate comprising (C). (C) can have cytostatic, anti-HIV, neuroprotective, anticonvulsant, antirheumatic, antiarthritic, dermatological, immunosuppressive, antiinflammatory, vasotropic, antiasthmatic, antiarteriosclerotic, immunostimulant, antipsoriatic, antiasthmatic, antiatiated cascade. A pharmaceutical composition comprising (C) can be used for the treatment of infections, MBL deficiency, cancer, immune and reproductive system disorders associated with chemotherapy, miscarriages, disorders associated with neutropaenia and human immunodeficiency virus (HIV). (C) is useful for the treatment of conditions of diseases and disorders in connection with immunosuppressive chemotherapy including, in
                                                                                                                                                                                                                                                                           Human, mannan binding lectin, MBL; immune system; immunosuppressive;
infection; cytostatic; anti-HIV; neuroprotective; anticonvulsant;
antirheumatic; antiarthritic; dermatological; immunosuppressive;
antiinflammatory; vasotropic; antiallergic; antiasthmatic;
antiinflammatory; vasotropic; antiallergic; antibacterial;
antialabetic; immunomodulator; cancer; immune disorder; chemotherapy;
reproductive system disorder; macarriage; neutropaenia; HIV; epilepsy;
human immunodeficiency virus; multiple sclerosis; myasthenia gravis;
chronic inflammatory demyelinating polyneuropathy; rheumatoid arthritis;
Baton-Lambert's syndrome; systemic lupus erythematosus; vasculitis;
Wegner's graaulomatosis; Sjogren's syndrome; autoimmune neutropaenia;
Crohn's disease; colitis ulcerous; asthma; septic shock syndrome;
atheroselerosis; immunodeficiency; Wiskott-Aldrich syndrome; SCID;
Kawasaki's disease; Guillain-Barre's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Production of human recombinant mannan binding lectin composition for treating disorders associated with chemotherapy, HIV, by transforming host cell culture with gene expression construct and cultivating culture.
                                                                                                                                                                                                                                           Human mannan binding lectin protein SEQ ID NO:1.
                       Disclosure; Page 60-61; 65pp; English
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99DK-00001508
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JENSEN I V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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20-OCT-1999;
                                                                                                                                                                                                     09-MAR-2001
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                                                                                                                                                              AAB36578;
721
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                                                                                               AAB3657
                                                                                RESULT
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240

AspCysValLeuLeuLeuLeuLysAsnGlyGlnTrpAsnAspValProCysSerThrSerHis

221

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180 900

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181

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GAAGCCTTCCTGGGCATCACTGATGAGACAGAAGGGCAGTTTGTGGATCTGACAGGA GluAlaPheLeuGly11eThrAspGluLysThrGluGlyGlyGlnPheValAspLeuThrGly AATAGACTGACCTACACAAACTGGAACGAGGTGAACCCAACAATGCTGGTTCTGATGAA AsnargleuThrTyrThrAsnTrpAsnGluGlyGluProAsnAsnAlaGlySerAspGlu GATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT

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particular infections which are seen in connection with implantation and/or transplantation of organs and diseases such as chronic inflammatory demyelinating polymeuropathy, multiple sclerosis, epilepsy, myasthenia gravis, Eaton-Lambert's syndrome, rheumatoid arthritis, systemic lupus erythematosus, vasculitis, Wegner's granulomatosis, sjogren's syndrome, autoimmune neutropaenia, Crohn's disease, colitis ulcerous, asthma, septic shock syndrome, psoriasis, toxic shock syndrome, hypo/agammaglobulinaemia including common variable immunodeficiency, Wiskott-Aldrich syndrome and severe combined immunodeficiency (SCID), Kawasaki's disease, and Guillain-Barre's syndrome. The present sequence represents human MBL, which is given in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                        present invention
        8X6666666666666888
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## Sequence 248 AA;

248	48				
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Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
5.48e-115	1321.00	100.00%	100.00%	96.78	4
Alignment Scores: Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:

## US-10-054-536-2 (1-747) x AAB36578 (1-248)

US-10-054-536-2 (1-747)	-536-	2 (1-747) x AAB36578 (1-248)
ζ۵	н	ATGICCCTGTTTCCATCACTCCCTCTCTCTCTGAGTATGGTGGCGGCAGCGTCTTACTCA 60
Db	Н	MetSerLeuPheProSerLeuProLeuLeuLeuLeuSerMetValAlaAlaSerTyrSer 20
δ	61	GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120
Db	21	GluThrValThrCysGluAspAlaGlnLysThrCysProAlaVallleAlaCysSerSer 40
δλ	121	CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG 180
Db	41	ProGlylleAsnGlyPheProGlyLysAspGlyArgAspGlyThrLysGlyGluLysGly 60
δλ	181	GAACCAGGCCAAGGCTCAGAGGCTTACAGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
Db	61	GluProGlyGlnGlyLeuArgGlyLeuGlnGlyProProGlyLysLeuGlyProProGly 80
οy	241	AATCCAGGGCCTTCTGGGTCACCAGGGCCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT 300
qu	81	AsnProGlyProSerGlySerProGlyProLysGlyGlnLysGlyAspProGlyLysSer 100
δλ	301	CCGGATGGTGATAGTAGCCTGGCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360
qq	101	ProAspGlyAspSerSerLeuAlaAlaSerGluArgLysAlaLeuGlnThrGluMetAla 120
٥'n	361	CGTATCAAAAAGTGGCTGACCTTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG 420
qq	121	ArgileLysLysTrpLeuThrPheSerLeuGlyLysGlnValGlyAsnLysPhePhebeu 140
δλ	421	ACCANTGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
qq	141	ThrasnGlyGluIleMetThrPheGluLysValLysAlaLeuCysValLysPheGlnAla 160
ò	481	TCTGTGGCCACCCCCAGGAATGCTGCAGAATGGAGCCATTCAGAATCTCAACAAGAG 540
qq	161	ServalalaThrProArgAsnAlaAlaGluAsnGlyAlaIleGlnAsnLeuIleIysGlu 180
λ	541	GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600
qa	181	GlualapheLeuGly1leThrAspGluLysThrGluGlyGlnPheValAspLeuThrGly 200
QY	601	AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA 660
Db	201	AsnargLeuThrTyrThrAsnTrpAsnGluGlyGluProAsnAsnAlaGlySerAspGlu 220
ογ	661	GATTGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCCAT 720
qq	221	AspCysValLeuLeuLeuLysAsnGlyGlnTrpAsnAspValProCysSerThrSerHis 240

GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120

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The invention relates to a methylotrophic yeast strain (I) comprising a DNA molecule encoding mannose-binding protein (MBP), protein disulphide isomerase (PDI), heat shock protein 47 (hsp47), and propyl-4-pytoxylase (P4H), where upon culturing (I) produces the MBP, PDI, hsp47 and P4H. (I) is useful for producing MBP comprising culturing (I) under conditions suitable for the secretion of MBP by the yeast where MBP is utilised in disposal of pathogenic organisms by opsoniasing pathogen or activating complement cascade. The methods utilising (I) result in high yields of MBP without the use of foetal calf serum, in a cost-effective manner. The present sequence relates to the amino acid sequence of human mannose-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methylotrophic yeast strain, useful for producing mannose-binding protein, comprises DNA molecules encoding the protein, protein disulfide isomerase, heat shock protein 47 and propyl-4-hydroxylase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; mannose-binding protein; MBP; methylotrophic yeast strain; protein disulphide isomerase; PDI; heat shock protein 47; hsp47; propyl-4-hydroxylase; P4H; pathogenic organism disposal; biocide.
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Matches:
Conservative:
Mismatches:
Indels:
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               241 LeuAlaValCysGluPheProile 248
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CIGGCCGICIGIGAGIICCCIAIC 744
                                                                                                                                                                          Human mannose-binding protein (MBP).
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                                                                                      AAU75574 standard; protein; 248
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                                                                                                                                                                                                                                                                                                                                                                                                             (APTA-) APTAGEN INC.
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Best Local Similarity:
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721
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CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAGGGG
            ProGlyIleAsnGlyPheProGlyLysAspGlyArgAspGlyThrLysGlyGluLysGly
                                                                                      AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCCAAAAAGGAGACCCTGGAAAAAGT
                                                                                                                              CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCA
                                                                                                                                            TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG
                                                                                                                                                                                                                                                                                                                        GluAlaPheLeuGlylleThrAspGluLysThrGluGlyGlnPheValAspLeuThrGly
                                                                                                                                                                                                                                                                                                                                                                    AsnArgLeuThrTyrThrAsnTrpAsnGluGlyGluProAsnAsnAsnAaGlySerAspGlu
                                          GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA
                                                        GluProGlyGlnGlyLeuArgGlyLeuGlnGlyProProGlyLysLeuGlyProProGly
                                                                                                  AsnProGlyProSerGlySerProGlyProLysGlyGlnLysGlyAspProGlyLysSer
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                                                                                                                                                                                                                                                                                                          GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA
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The invention relates to a novel pharmaceutical composition comprising additives and at least 200 micrograms/ml protein containing material where mannan binding lectin (MBL) and/or MBL variant constitute at least 25% {w/w} of total protein, or comprising at least 400 micrograms/ml MBL associated serine protease(s) (MASP) or its fragments, particularly MBL-associated serine protease(s) (MASP) or its fragments, particularly MSP-1, MASP-2 or MASP-3 having respectively the 699, 686 or 728 amino acid sequence fully defined in the specification. The MBL preferably has the 248 sequence fully defined in the specification or it's fragment and may be purified naturally occurring human serum MBL or recombinant and immunostimulant activities. The composition can be used to treat a clinical condition, particularly an infection, especially where the individual has a subnormal MBL level. The composition may be used to treat immunocompromised conditions. This sequence represents the 248 amino acid mannan binding lectin protein of the invention. 120 180 240 100 360 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAGT 300 120 9 20 40 9 80 nceutical composition containing mannan binding lectin or its is useful to treat clinical conditions, particularly infection, 1 ATGLCCCTGTTTCCATCACTCCCTCTCCTTCCTGAGTATGGTGGCGCGTCTTACTCA MetSerLeuPheProSerLeuProLeuLeuLeuLeuSerMetValAlaAlaSerTyrSer GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT GluThrValThrCysGluAspAlaGlnLysThrCysProAlaValIleAlaCysSerSer CCAGGCATCAACGCCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGG ProGlyIleAsnGlyPheProGlyLysAspGlyArgAspGlyThrLysGlyGluLysGly GAACCAGGCCAAGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA GluProGlyGlnGlyLeuArgGlyLeuGlnGlyProProGlyLysLeuGlyProProGly ProAspGlyAspSerSerLeuAlaAlaSerGluArgLysAlaLeuGlnThrGluMetAla CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAGCTCTGCAAACAGAAATGGCA 248 248 0 0 0 0 0 Length: Matches: Conservative: Mismatches: Indels: (1-248)English and immunosuppressive conditions. US-10-054-536-2 (1-747) x ADE87458 5.48e-115 1321.00 100.00% 100.00% 96.78% NO 1; 44pp; Best Local Similarity: pharmaceutical SEQ ID Sequence 248 AA; Percent Similarity: Alignment Scores: 61 21 121 41 181 61 241 81 101 301 variant Query Match: DB: g à à Ωp ŏ q à Ωp ö Dp g à

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ArglleLysLysTrpLeuThrPheSerLeuGlyLysGlnValGlyAsnLysPhePheLeu

CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG

361

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GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAGGGGCAGTTTGTGGATCTGACAGGA 600

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MBP is a soluble lectin-like molecule which is synthesised in hepatocytes and released into the bloodstream. Human MBP binds carbohydrate and can selectively recognise configurations of high mannose, fucose or N-acetylglucosamine which are present on pathogens. Interaction of MBP with mannose-rich pathogens enhances clearance of the pathogens by phagocytosis or results in activation of complement. Sequences (cDNA and genomic DNA) coding for human MBP have been isolated. (Updated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       mannose; lectin;
fixing domain; anti-viral agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              formation
                                                                    GATTGTGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACT
AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125. .248
/label= Carbohydrate-binding domain
/note= "mannose-binding domain is within this region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63. .101
/label= complement-fixing_domain
/note= "collagen-like segment with Gly-X-Y repeats"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "corresponds to AAC codon in AAQ53529"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "corresponds to GCC codon in AAQ53529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "corresponds to GAT codon in AAQ53529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              consistent
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    .62
    /note= "Cysteine-rich region,

                                                                                                                                                                                                                                                                                                                                                                                                                                        human MBP; N-acetylglucosamine; fucose; carbohydrate binding domain; complement
                                                                                                                                                                                  744
                                                                                                                                                                                                       .ocation/Qualifiers
                                                                                                                                                                                     CTGGCCGTCTGTGAGTTCCCTATC
                                                                                                                                                                                                                                                                                       standard; protein; 248
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                                                                                                                                                                                                                                                                                                                                                                                                         Human Mannose-Binding Protein.
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89US-00417822.
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N-PSDB; AAQ53529, AAQ53530.
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(first entry)
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13-JUN-1994
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The invention relates to cancer inhibiting agents that contain an active component, mannan-binding protein (or the gene encoding it). Mannan-binding protein (MBP) has carcinostatic activity, and can be used as the active component in anticancer agents for inhibiting tumour growth and suppressing the proliferation of a cancer into surrounding tissue. Alternatively, the gene encoding MBP may be delivered to the tumour in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carcinostatic agent containing mannan-binding protein - inhibits cancer growth and proliferation into surrounding tissues.
    101 ProAspGlyAspSerSerLeuAlaAlaSerGluArgLysAlaLeuGlnThrGluMetAla
                                                                                                       ThrAsnGlyGluIleMetThrPheGluLysValLysAlaLeuCysValLysPheGlnAla
                                                                                                                                                           221 AspCysValLeuLeuLeuLeuLysAsnGlyGlnTrpAsnAspValProCysSerIleSerHis
                                                                                          ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC
                                                                                                                                           TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG
                                                                                                                                                                                             GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA
                                                                                                                                                                                                             GluAlaPheLeuGlyIleThrAspGluLysThrGluGlyGlnPheValAspLeuThrGly
                                                                                                                                                                                                                                               AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAA
                                                                                                                                                                                                                                                                                               GATTGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mannan-binding protein; MBP; carcinostatic; anticancer agent; tumour;
                                                                                                                                                                                                                                                                                                                                                  744
                                                                                                                                                                                                                                                                                                                                                                            248
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                                                                                                                                                                                                                                                                                                                                                                                                                               Ä.
                                                                                                                                                                                                                                                                                                                                                                         LeuAsnValCysGluPheProIle
                                                                                                                                                                                                                                                                                                                                                   CTGGCCGTCTGTGAGTTCCCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                               AAY03769 standard; protein; 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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                                                                                                                                                                                                                                                                                                                                                                        activity, and gene encoding it useful for production of transgenic animals and of antibodies for screening potential drug molecules.
                                                                                                                                                                                                                                                                                                                                                            New collectin of human origin having antibacterial and antiviral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
44
84
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
                                                                                                                            Collectin; human; antibacterial; antiviral; MBP,
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                         Ą.
                        standard; protein; 248
                                                                                                    Human MBP amino acid sequence.
                                                                                                                                                                                                                                99WO-JP004552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 248 AA;
                                                                                                                                                                              WO200011161-A1.
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                24-AUG-1999;
                                                                                                                                                                                                                                                         24-AUG-1998;
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                                                                           20-JUN-2000
                                                                                                                                                                                                                                                                                                           Wakamiya N;
                                                AAY77988;
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(revised)

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25-MAR-2003
29-JUN-1990
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plasmid or viral vector (especially in a vaccinia or adenovirus vector). The MBP may be human MBP, or derived from it by addition, deletion and/or substitution of one or more amino acid residues. The agents containing the MBP can be used for effective treatment of malignant tumours (including solid tumours) by direct application to the tumour. The present sequence represents a MBP sequence
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Conservative:
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plasmid or vir
The MBP may be
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for deriving diagnostic antibodies.
                             (PMBP)
                               protein
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Mismatches:
Indels:
                               sequence of human mannose binding
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Best Local Similarity:
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infections, used
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                                                                                                                                                                                                                                                                                                                                         Ezekowitz RAB;
                                                                                       Human mannose
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                                                                    CTTCCTGGGCATCACTGATGAGAGACAGAAGGGCAGTTTGTGGGATCTGACAGGAAATAG
                                                                                                                                              ACTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTG
                                                                                                                                                                                                   TGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGC
       GTGATAGTAG-CCTGGCTGCCTCAGAAAAAAAAGCTCTGCAAACAGAAATGGCACGTATC
                                      AAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAAT
                                                 |||||
| 122 InLysCys-LeuThrPheSerLeuGlyLysGlnValGlyAsnLysPhePheLeuThrAsn
                                                                                                    GCCACCCCCAGGAATGCT-GCAGAGAATGGAGCCATTCAGAATCTCAAGGAGGAAGC
                                                                                                              pProProFroGlyMetAlaAlaGluAsnGlyAlaIleGlnAsnLeuIleLysGluGluAl
                                                                                                                                                                             Pig; serum; lectin; phosphomannan affinity; Hansunela capsulata;
physiologically active substance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New pig serum lectin gene encoding phosphomanna
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                                                                                                                                                                                                                                                                                 AAB15401 standard; protein;
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N-PSDB; AAA70738.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCGGCGTCTTACTCA
                                                                                      GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT
                                                                                                       CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAAGGG
                                                                                                                                                                   GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGGCCTCCAGGA
                                                                                                                                                                                                                           241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGGCCCTGGAAAAGT
                                                                                                                                                                                                                                                                                         301 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGA-----AAAGCTCTGCAAACAAA
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|ThrGlyGlyArgMetThrTyrSerAsnTrpLysSerAsnGluProAsnAspHisGlySer
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(1-249)
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GlySerSerLeuCysLeuAlaThrGlyGlnGlyLeuArgGlyLeuGlnGlyProPro 232
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                                                                                                                                                                                                                                                                                                                                               173 His***ValAlaGlyGluSerPhePheGlySerAspHisTrpLeuIleGlyCysAla 192
                                                                                                                                                                                                                                                                                                                                                                                                             GlyGlyGluGlnGluTrpSerIleGluLeuLeuGlyLysLysLysArgValThrAlaThr 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAAAGTTGGGGCCTCCAGGAAATCCAGGCCTTCTGGGTCACCAGGACCAAAGGGCCAA
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                                                                                                                                                                                                                   133 ThrLysLeuPheValAspSerLeuGlySerHisIleSerThrGlnGluLeuGlyValCys
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Leu***SerLeuArgSerGluLeuAspHisThrLysLysLeu***ProPheSerLeuGly
                          dluProGlyLeuGlyGlnValSerValAlaSer***IleSerThrSerGlyArgCysSer
                                                                                        93 SerLysSerValLeuGluProAlaThrArgGlyLeuLysHisArgLeuGlyGluAlaPro
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                                                                                                                                                     113 LeuSerSerGlyProMetLeuHisSerGluGlnProLeu***AsnAlaIleAlaSerLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to polymucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymerides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, nematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCAGGCATCAACGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAGGGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAAACIGIGACCIGIGAGGAIGCCCAAAAGACCIGCCCIGCAGIGAIIGCCIGIAGCICT 120
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R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA
   haematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                     Xu C,
, Chen
vaccine; peptide therapy; stem cell growth factor; haemato
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.
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1155
31
60
150
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J, Zhang J, Ren F,
Goodrich R;
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 20; Page 321; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, A
Wang D, Wang J
Wejhrman T, G
                                                                                                                                                                                                         2000US-00560875.
2000US-00598075.
2000US-00620325.
2000US-00654936.
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2000US-00693325.
2000US-00728422.
                                                                                                                                                             05-FEB-2001; 2001WO-US004098
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727.00
46.97%
39.14%
53.26%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                      Zhao QA, ''
'Yang Y,
                                                                                                                                                                                                                                                                                                                                                                     Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAK52878
                                                                                                WO200157190-A2
                                                                                                                                                                                                                         20-JUN-2000; 2
19-JUL-2000; 2
01-SEP-2000; 3
                                                                                                                                                                                                                                                                        15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 409
                                                                  Homo sapiens
                                                                                                                                                                                           03-FEB-2000;
27-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
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Ma Y, Zh
Xue AJ,
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272 393 292 453

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312 513 573 352 633 372 693 392

Score:

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The present sequence is the protein sequence of a novel form of human surfactant protein D (SP-D) that is expressed in endothelial cells, inhibits oxidation of low density lipoprotein and protects endothelial cells, calls from oxidative damage. The andothelial form polypeptide lacks 93 amino acids compared to the lung form of SP-D and has only 28 Gly-Xaa-Xaa repeats as compared to 57 in the lung form of SP-D much bench on the invention provides a novel method of diagnosing a percon's susceptibility for having an increased risk for the development of atherosclerosis by masuring the amount of SP-D in plasma and serum samples. An increased risk for the development of atherosclerosis in a human is considered at a detected serum or plasma SP-D concentration below 1104.6 mg/ml, in the particular below 743 mg/ml, and especially below 370 mg/ml or 152.7 mg/ml. SP-D, or a nucleic acid encoding it, can be used to prevent or treat an atherosclerosis related disease such as stroke, kidney failure, and interest and process and process of the prevent or treat an atherosclerosis related disease such as stroke, kidney failure, and myocardial infarction, and to treat obesity
                                                                              Human; surfactant protein-D; SP-D; atherosclerosis; antiarteriosclerotic;
antidiabetic; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleotide sequence encoding surfactant protein-D, useful for preparing a composition for preventing or treating diabetes or
                                                                                                                                                                                                                                                                                                                                     .58, .282
|abel= Carbohydrate_recognition
                                              Human surfactant protein-D (endothelial form).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tornoe
                                                                                                                                                                                                                                                                                      note= "N-glycosylated"
                                                                                                                                                              location/Qualifiers
                                                                                                                                                                                                         12. .45
||abel= N-terminal
|6. .129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Madsen J,
                                                                                                                                                                                                                                                        label= Collagen
                                                                                                                                                                          1. .21
/label= Leader
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 3; Fig 1; 78pp; English.
                                                                                                                                                                                                                                                                                                     30. 157
|abel= Neck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-OCT-2001; 2001US-0330664P.
27-DEC-2001; 2001US-0342372P.
                                                                                                                                                                                                                                                                                                                                                                                                                                               25-OCT-2002; 2002WO-DK000711
               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-421403/39.
N-PSDB; ACC57755.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HOLM/) HOLMSKOV U.
(LYST/) LYSTER G L.
(MADS/) MADSEN J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TORNOE I.
                                                                                                                                                                                                                                                                                                                                                                                   WO2003035683-A2
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                                                                                                                              Homo sapiens
               28-JJL-2003
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                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                     Domain
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                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                       Region
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Length: Matches: Conservative: Mismatches:

1.39e-35

474.00 52.65% 40.28%

> Percent Similarity: Best Local Similarity:

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140 AlaLeuGlnGlyGlnValGlnHisLeuGlnAlaAlaPheSerGlnTyrLysLysValGlu 159
                                                                                                                                                                      TGTAGCTCT-----CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACC 165
                                                                                                                                                                                                                            204
                                                                                                                                                                                                                                                                                                                                  294
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                                                                                                                    GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCA------GTGATTGCC 111
                                                                                                                                                                                                                                                                             -----CCTGGAAAGTTGGGGCCTCCA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetLeuLeuPheLeuLeuSerAlaLeuValLeuLeuThrGln---ProLeuGlyTyrLeu 19
                                                                                                                                                                                                                                                   79
                                                                                                                                                                                                                                                                                                 80 GlnAladlyProValGlyProLysGlyAspAsnGlySerValGlyGluProGlyProLys 99
                                                                                                                                                                                       220 LeuSerMetThrAspSerLysThrGluGlyLysPheThrTyrProThrGlyGluSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGICCCTGITTCCATCACTCCCTCCTTCTCCTGAGTATGGTGGCAGCGTCTTACTCA
                                                                                                                                              GluAlaGluMetLysThrTyrSerHisArgThrThrProSerAlaCysThrLeuValMet
                                                                                                                                                                                                                            -- CAAGGGCTCAGAGGC
                                                                                                                                                                                                                                                                                                                             238 GGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGAGACCCTGGA---
                                                                                                                                                                                                                                                                                                                                                                                 295 AAAAGTCCGGATGGTGATAGTAGCCTG-----GCTGCCTCAGAAAGAAAAGCT----
                                                                                                                                                                                                                                                                                                                                                                                                                                    -CTGCAAACAGAAATGGCACGTATCAAAAAGTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           439 ACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGCCACCCCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   610 ACCTACACAAACTGGAACGAGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGTGTA
  38
 Indels:
Gaps:
                                       (1-282)
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                                                                                                                                                                                                                         166 AAGGGAGAAAAGGGGGAACCAGGC
                                                                                                                                                                                                                                                                         205 TTACAGGCCCC------
                                       US-10-054-536-2 (1-747) x ABR42241
 34.73%
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                                                                                                                                                                                                                                                     The invention relates to polynucleotides encoding a new collectin of human origin. The collectin can be used as an antibacterial and antiviral agent and for screening potential drug molecules. The new collectin can be produced by standard recombinant methodology. The present sequence represents a human SP-D, used in homology studies with collectin
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                                                                                                                                                                                             New collectin of human origin having antibacterial and antiviral activity, and gene encoding it useful for production of transgenic animals and of antibodies for screening potential drug molecules.
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                  Collectin; human; antibacterial; antiviral; SP-D.
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Human SP-D amino
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The invention relates to a method of treating conditions associated with lipid oxidation, acute lung injury, atherosclerosis, inhibiting or reducing microbial contamination, preventing microbial proliferation, contamination or colonisation, and preventing spoilage of foods, cosmetics and medications. The method involves using an antioxidant or antimicrobial lung surfactant protein compound. The method is also useful for treating adult respiratory distress syndrome and hyperoxic lung injury. The surfactant proteins are advantageous over antioxidant ingredients such as butylated hydroxy toluene (BHT) or antimicrobial products, since they are derived from animal sources, are edible and are non-toxic. The present sequence represents human lung surfactant protein D used in the method of the invention
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GlyValProGlyGluArgGlyValProGlyAsnThrGlyAlaAlaGlySerAlaGlyAla
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Homo sapiens

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The invention relates to a recombinant surfactant protein D (rSPD) (n/CRD) polypeptide (I), or its fragment, homologue, variant or derivative, for use in treatment or prophylaxis of a disease. (I) is useful for treating an individual suffering from a disease or preventing the occurrence of a disease in an individual, where the disease comprises an inflammatory a disease, preferably eczema or an inflammatory lung disease (selected from neonatal chronic lung disease, neonatal respiratory distress syndrome (RDS), adult respiratory distress syndrome, chronic obstructive airways disease (COPD), asthma, cystic fibrosis, pulmonary fibrosis, emphysema, interstitial inflammatory lung disease, sarcoidosis, pneumonia, chronic inflammatory lung disease, neonatal chronic inflammatory lung disease, and allergy (see ACC48168 for a detailed description of all the diseases surfactant protein (SP-D)
                                                                                                                                                                                                                                                                                                                                                                                                             Novel recombinant surfactant protein D, termed rSPD n/CRD polypeptide, or its fragment, homolog, variant or derivative, useful for treating inflammatory diseases, asthma, allergy, or atherosclerosis.
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2002GB-00009619.
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                                                                                                                                                                              GAAGATTGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCC 717
The present sequence is bovine conglutinin (bCG), from which a novel recombinant bCG can be prepared. The recombinant bCG comprises a truncated collagen region of formula Gly-Xaa-Xaa-Gly-Xaa-Xaa (where Xaa is any amino acid), and the neck and sugar chain recognition regions of natural bCG. The recombinant bCG has antiviral activity, i.e. virus neutralising activity, and can be used to treat viral diseases,
                                                                                      GAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACA
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                                            GCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC
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                                                                                                                                                                                                                            CATCTGGCCGTCTGTGAGTTC 738
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treatment; disease; influenza A.
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         Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers
1. 747
/organism="Homo sapiens"
/mol type=""genomic DNA"
/db xref="taxon:9606"
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive
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                                                                                                                                                                        Score 678; DB 29;
Pred. No. 3.3e-180;
0; Mismatches 69;
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/gene="MBL2"
/locus_tag="HCM4840"
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Best Local Similarity 90.8%;
Matches 678; Conservative
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RESULT 2 AY413287

747 bp DNA linear GSS 17-DEC-2003 Pan troglodytes MBL2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence. ö 120 300 360 120 180 240 420 361 NINININININININININGGCTGACCTTCTCTGGGGCAACAACTTGGGAACAAGTTCTTCCTG 420 480 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAGGGG 180 Pan troglodytes (chimpanzee)
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
I (Dases I to 747)
Clark, A.G.; Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriara, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M. 09 9 Clark.A.G. Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Clark.A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wangy,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
Location/Qualifiers 1 ALGICCCTGTTTCCATCACTCCCTCTCTCTCTGAGTATGGTGGCGGCGTTACTCA GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 121 CCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGGGAAAAAGGG 1 ATGICCCIGITICCATCACTCCCTCTTCTCCTGAGIAIGGTGGCAGCGTCTTACTCA GAACCAGGCCAAGGCTCAGAGGCTTACAGGCCCCCCTGGAAAGTTGGGGGCCTCCAGGA GAACCAGGCCAAGGCTCAGAGGCTTACAGGGCCCTCCTGGAAAGTTGGGGCCTCCAGGA AATCCAGGCCTTCTGGGTCACCAGGACCAAAAGGCCCAAAAAGGAGCCCTGGAAAAAGT 241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAGAAAGGAGACCCTGGAAAAAGT CGTATCAAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTGCTG ., 0 Length 747; Indels DB 29; 89.9%; Score 671.6; DB 29; 90.2%; Pred. No. 2.1e-178; live 0; Mismatches 73; 1. .747
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/db\_xref="taxon:9598"
<1. .774
/gene="MBL2"
/locus\_tag="HCM4840" Science 302 (5652), 1960-1963 (2003) 14671302 AY413287.1 GI:39769249 674; Conservative Similarity gene trios AY413287 Query Match Best Local Si Matches 674, 301 61 121 181 181 241 361 421 301 LOCUS DEFINITION ORGANISM REFERENCE AUTHORS REFERENCE AUTHORS ACCESSION TITLE JOURNAL VERSION KEYWORDS SOURCE gene JOURNAL PUBMED FEATURES TITLE COMMENT

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mRNA sequence. _____BF537636
BF537636
BF537636.1 GI:11625004
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bumanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musil
Chases 1 to 735)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Ford, M.A., Tanembaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCC 480
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This sequence was made by sequencing genomic exons and ordering them based on alignment.

Location/Qualifiers
                                                                                                                                          AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAAATGCTGGTTCTGATGAA
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                            TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAG
                                            TCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCGTTCGGAATCTCATCAAGGAG
                                                                                   GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA
                                                                                                   GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA
                                                                                                                                                                    AATAGACTGACCTACACAAACTGGAACGAGGTGAACCCAACAATGCTGGTTCTGATGAA
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Pred. No. 4.2e-88;
0; Mismatches 237; Indels
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/locus_tag="HCM4840"
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larity 66.3%;
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 828)
Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
TACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAG
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Bukaryotti, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

I (basea I to 36.7)

Xu,X., Huang,J., Xu,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,M., Shen,X., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.

Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver

Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
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Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
           AV660023 GLC Homo sapiens cDNA clone GLCGDC05 3', mRNA sequence
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Not! Site 2: Sali; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1:3 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

44.8%; Score 335; DB 10;

Best Local Similarity 71.5%; Pred. No. 3.3e-83;

Matches 511; Conservative 0; Mismatches 195;
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           column: 04
                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
Plate: LLAM9526 row: o column:
High quality sequence stop: 757
Location/Qualifiers
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Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
Wang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
Direct Submission
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xu,C.S., Li,W.O., Li, Y.C., Han, H.P., Wang,G.P., Chai,L.Q.,
Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F., Zhao,L.F., Ma,H.,
Mang,L., Wang,S.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
Liver regeneration after PH
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319 Trosaaagaagrartrorgagcagrorraaaaagargaccrrgacagagrgaaggccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-JUN-2003) Henan Bioengineering Key Lab, Henan Nor
University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002,
                                                                                                                                                                                                       139 gaaaagraggaccracaggacccccagggaarccggggrraaaaggagcagragagccga
                                                                                                                                                                                                                                                                                 199 AAGGAGACCGTGGGGACAGAGCAGAATTTGATACTAGCGAAATTGATTCAGAAATTGCAG
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/note="liver regeneration-related protein LRRG037"
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/db_xref="GI:33086526"
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Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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LOCUS
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JOURNAL
REFERENCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bunanalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 657)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                          AI255533 657 bp mRNA linear EST 12-NOV-195 ui55f12.yl Sugano mouse liver mlia Mus musculus cDNA clone IMAGE:1886351 5' similar to gb:D11440 Mouse mRNA for P28a subunit of Ra-reactive factor, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL , contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:970675
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WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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/mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
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Location/Qualifiers
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/clone="IMAGE:1886351"
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KDGHDGAKGEKGEPGQGLRGLQGPPGKVGPAGPPGNPGSKGATGPKGDRGESVEFDTT
NIDLEIAALSEELRAMKWYLLSMSRNVGKKYFMSSYRRMPLNRAKALCSELQGTVAT
PRNAEENRAI OWVAKDVAFLGITDQRTENVFEDLTGNRVRTYWNBGRLSLRGPELHG
PAANGYYTTESSEDFRI PPTERTAKDGCALDPYEQSLIHAATESKANSENQHYTLEK
QSVHISVVSVEFLVNLQMFAVTVSSHITRGNRSLIPGLTHBDFPHKQADSPELLT
WLDRMASEPAGCSGLPSCSTRIVDVCQVYLDTMTMFV"
translation="MSLFTSFLLLCVLTAVYAETLTEGAQSSCPVIACSSPGLNGFPG/
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                                                                                                                                            Score 301.4; DB 11; Length 1162; Pred. No. 1.3e-73; 0; Mismatches 167; Indels 0;
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llarity 70.6%;
Conservative
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Matches 401
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HTC 26-JUL-2003
                                                                                                                       Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                1 (bases 1 to 1162)

Xu,C.S., Li,W.Q., Li,Y.C., Ma,H., Wang,L., Wang,S.F., Han,H.P.,
Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F.
Zhao,L.F., Shi,J.B., Rahman,S., Wang,Q.N. and Zhang,J.B.
Liver regeneration after PH.
                                        linear
                                                      cds.
                                                        complete
                                        mRNA
                                1162 bp
Rattus norvegicus Ab2-001 mRNA,
AY325178
37325178.1 GI:33086533
HTC.
                                                                                                                                                                                                                                                                                                                   (bases 1 to 1162)
                                                                                                                                                                                              Rattus.
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VERSION
KEYWORDS
SOURCE
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                                                   DEFINITION
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JOURNAL
REFERENCE
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AUTHORS
RESULT 8
AY325178
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KDGHDGAKGEKGEPGQGLRGLOGPPGKVGPAGPPGNPGSKGATGPKGRGESYBFDTT
NIDLEIAALRSELRAMRKWYLLSMSENVGKKYFMSSVRRMPLNRAKALCSELGGTVAT
PRNAEENRATONVAKOVAFLGTTDQRTENVFEDITGNRYTYTWNBGSTLSLRGPFLHG
PAANSVYXTPSSSDTENI PPTEFTAKGCALDPYGGSLIHAATESKANSENGHYTLEK
QSVHISVYSVBFLYDGAVTAVSSHTTRGNRRSLTPGLTHEDPPHKQADSPSLELTG
MLDRMASEPAGCSGLPSCSTRIVDVCQVYLDTMTMFV"
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02, P.R.
                                                                                                                                                                                                                                                                                                           translation="MSLFTSFLLLCVLTAVYAETLTEGAQSSCPVIACSSPGLNGFPG"
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Ku,C.S., Li,W.Q., Li,Y.C., Ma,H., Wang,L., Wang,S.F., Han,H.P.,
Wang,G.P., Chai,L.Q., Yuan,J.Y., Yang,K.J., Yan,H.M., Chang,C.F.
Zhao,L.F., Shi,J.B., Rahman,S., Wang,O.N. and Zhang,J.B.
Direct Submission
Submitted (16-UNN-2003) Henan Bioengineering Key Lab, Henan Norm
University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, Pchina
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                                                                                                                      Location/Qualifiers
1. 1162
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/db_rref="taxon:10116"
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                                                                                                                                                                                                                                          /codon_start=1
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/db_xref="GI:33086534"
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AV660367 GLC Homo sapiens cDNA clone GLCGGH07 3', mRNA sequence.
AV660367
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
685 TACAGGACCCNCAGGGAATCGGGGTTAAAAGGAGCAGTGTACCGAAAAGGAGACCGTGNG 626
                                                                                                                                                         355 ATGGCACGTATCAAAAGTGGCTGACCTTCTCTGGGCAAAAAGTTGGGAACAAGTTC 414
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/clone="GLCG407"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 GGGGAAGACTGTGTGGTGATCTTGGGAAATGGCAAGTGGAACGGATGTCCCCTGCTCTGAC
                                                                                                   GACAGAGCAGAATTTGATACTAGCGAAATTGATTCAGAAATTGCAGCCCTACGATCAGAG
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                                                     446 cagggerrergresceaereceaggaargergaggaaaaerecggecarecagaaagregee
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong,
201203, P. R. China
                                                                                                                                                                                                                                                             TTCCTGACCAATGGTGAAATAATGACCTTTGAAAAAGTGAAGGCCCT
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This clone is available at CHGC in Shanghai.
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Fax: 86-21-50801922
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// NOCE="Organ: liver: Vector: pWE185-FI3; Site 1: DraIII (ACCTGTGTG); Ist strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTTGGCTACTGG], digested and cloned into distinct DraIII sites of the pWE185-FL3 vector (5' site CACTGTGTG, 3' site CACTGTGTG, 3' site CACTGTGTG, be used to isolate the CDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCTGCTCTAAAAGCTGCG and 3' end primer CGACCTGCAGGCACA."
                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 869)
Marram, Hillier, Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                             AI195233

ui62c03.xl Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1886980 3' similar to gb:X15422 cds1 MANNOSE-BINDING PROTEIN
C PRECURSOR (HUMAN); gb:D11440 Mouse mRNA for P28a subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
Contact: Marxa MyMouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                            Ra-reactive factor, complete (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 208; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_rege="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver mlia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39.1%; Score 292.4; DB 9; 67.0%; Pred. No. 3.7e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .869
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 428.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:1886980"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: custom primer used
                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="female"
                                                                                                                                                                                                 AI195233.1 GI:3747839
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                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:971304
                                                                                                                                                                         AI195233
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                AI195233/c
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JOURNAL
                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
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/clone_libe_Sugano mouse liver mlia"
/clone_libe_Sugano mouse liver mlia"
/note="Organ: liver; Vector: pWE18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); ist Etrand cDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTTTTTTTTTTTTT]; double stranded cDNA was
ligated to a DraIII adaptor [GTTGGCTACTGG], digested
and cloned into distinct DraIII sites of the pWE18S-FL3
vector [5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAAGCTGGG and 3' end
primer CGACCTGCAGCTCGAGCACA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 CCTTCTGG-GTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCCGGATGG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACTCCCAGGAATGCTGAGGAAACTCGGCCATCCAGAAAGTGGCCAAAGATATTGCCTA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAAAAAGGGGGAAACCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCCGGGNGTTAAAAGGAGCAGTGGACCGAAAGGAGACCCTGGGGACAGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGATAGTAGCCTGGCTGCCTCAGAAAAAAGCTCTGCAAACAGAAATGGCACGTATCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAGGGCTCAGAGGCTTACAGGGCCCCCTGGAAAGTTGGGGGCCTCCAGGAAATCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  731 CAAGGICAANAGGCTTGCAAGGCCTCCTGGAAAAGTAGGACCTACAGGACCCCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                611 İGATACTAĞCGAAATTGATTCAGAATTGCAĞCCCTACGATCAĞAGCTĞAGAGCCCTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAGTGGCTGACCTTCTCTCTGGGCAACAAGTTGGGAACAAGTTCTTCCTGACCAATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         551 AAACTGGGTGCTCTTCTCTCTGAGTGAAAAGTTGGAAAGAAGTATTTTGTGAGCAGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCAAGTTCCAGGCCTCTGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  491 TAAAAAGATGAGCCTTGACAGAGTGAAGGCCCTGTGCTCCGAATTCCAGGGCTCTGTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGGATCTGACAGGAAATAGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 789;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.9%; Score 290.4; DB 9; Length 69.8%; Pred. No. 1.3e-70; Live 0; Mismatches 184; Indels
                                                                                                       1. .789 /organism="Mus musculus"
                                                            486.
                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:1450922"
MGI:924238
Seq primer: custom primer used
High quality sequence stop: 486
Location/Qualifiers
                                                                                                                                                                                                                                                                 /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL"
                                                                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 38.9
Best Local Similarity 69.8
Matches 432; Conservative
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Mus musculus
Bukaryota, Metazoa; Chordata, Craniata, Vertebrata; Buteleostomi,
Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; I to 789)
Marmal, Dases 1 to 789)
Marrah, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                       233
                                                                                                                                                                                                                                                                                                                                293
                                                                                                                                                                                                                                                                                                                                                             TCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAACCCTGG 120
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                                                                                                                                                                                                                                                                                    9
                            /clome_lib="GLC"
/note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
XhoI:
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ud67a02.x1 Sugano mouse liver mlia Mus musculus cDNA clone
IMAGE:1450922 3' similar to gb:D11440 Mouse mRNA for P28a subunit
of Ra-reactive factor, complete (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                          234 TCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAAGGGCCAAAAAGGACCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 AATGGCACGTATCAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         307 CAAGGAGGAAGCCTTCCT-GGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCT
                                                                                                                                                                                                                                   AAAGGGGGAAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCC
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                                                                                                                                                                                             Gaps
                                                                                                                                                                                             52;
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                                                                                                                                                 Length 367
                                                                                                                                          Score 291; DB 9; Length 36 Pred. No. 5.4e-71; 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
444 Forest Parkway, Box 8501, St. Louis,
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTTCCTGACCAATGGTGAATAATGACCTTTG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
Unpublished (1996)
         /lab host="SOLR"
                                                                                                                                            39.0%;
86.9%;
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AUTHORS
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'clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tissue_type="embryonic body between diaphragm region and
          Yokohama,
                                                                                                                               Riken
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, NELihttp://genome.gsc.riken.go.jp, Tel:81-45-503-922, Fax:81-45-503-9216) cDNA library was prepared and sequenced in Mouse Genome in Richard and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Rike Genomic Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="mannose binding lectin, liver (A) (MGD|MGI:96923,
GB|NM_010775, evidence: BLASTN, 99%, match=922)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAAGGGGGAAACCAGGCCAAGGGCTCAGA
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Please visit our web site for further details.
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Pred. No. 3.5e-69;
                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM_DB:9430039D04"
/db_xref="MGI:2398998"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="12 days embryo"
                                                                                                                                                                                                                                                            URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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68.0%;
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Matches 416; Conservative
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                                                                                                                                                                                                                  Mus musculus 12 days embryo embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:9430039D04 product:mannose binding lectin, liver (A), full insert sequence.
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Adachi, J. Aizauzo,
Adachi, J. Aizauzo,
Fukuda, S. Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramcto, K., Hiracka, T., Hirozane, T.,
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,
Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Nakamuza, M., Nishi, K., Nomuza, K., Niwazaki, A., Murata, M.,
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabo, Y., Tagama, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format Genome Res. 10 (11), 1757-1771 (2000)
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Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                   linear
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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HTC; CAP trapper.
Mus musculus (house mouse)
                                                                        CTGTGAATTCTCTGACTGA 173
                       CTGTGAGTTCCCTATCTGA
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Mammalia; Eutheria;
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USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4366
Fax: 402 762 4360
Small: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and minmatch 12 options.
PCR PRIMERS
PCR PRIMERS
                                                               423
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                                                         364 GAAGCTGGCAAATATGGAGGCAGAGATAAGGATCCTGAAATCAAAACTGCAGCTAACCAA
                                                                                                                                                                                                                                                489 CACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAAGCCTT
                                                                                                                                                                                                                                                                                                                                                      604 CCTAGGCATCACGGACGAGGCGACTGAAGGGCAGTTCATGTACGTGACAGGGGGGGCT
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                                                                                                                                                                       CCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAATAGACT
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Plate: 83 row: O column: 15
Seg primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
1..557
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This clone has the following problem: frame shifted.
                                                                                                                                                                     HTC 20-SEP-2002
Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGGAACCAGG------CCAAGG 194
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                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (06-AUG-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X., Hulyk, S.W., Hale, S.M.,
S., Martin, R.G., Muzny, D.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amgebom.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.
Richards, S., Gibbs, R.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIH-MGC Project URL: http://mgc.nci.nih.gov
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/clone="IMAGE:4193682"
/clone="IMAGE:4193682"
/clone_lib="NCI GGAP_SG2"
/lab_host="DH10B"
/note="Vector: pGMV-SPORT6"

    .898
    /organism="Mus musculus"
/mol_type="mRNA"
    /strain="FVB/N"

                                                                                                                                                                                  Mus musculus, Similar to
IMAGE:4193682, mRNA.
                                                                                                                                                                                                                     BC012245
BC012245.1 GI:15126625
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                                                                     829 rrcccagccrca 840
                                    TTCCCTATCTGA
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Best Local S
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Job time : 2549 secs
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Mus musculus cDNA clone IMAGE:5053406 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 788)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.9
                    /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab host="PH10B"
/clone_lib="MARC 4BOV"
/note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sal1;
Library made from pooled tissue from day 20 and day 40 embryos."
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                     Score 268.4; DB 10; Length 557; pred. No. 1.7e-64; 0; Mismatches 167; Indels 6;
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organism="Bos taurus"
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68.9%;
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BI147944.1
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/strain="FVB/N"
/strain="FVB/N"
/db xref="taxon:1000"
/clone="INAGE:5053406"
/lab host="UPH10B (T1 phage-resistant)"
/clone lib="NCI CGAP_Li9"
/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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                                                                                                                                                                                                                                                                                                                                                   35.9%; Score 268; DB 12; 72.4%; Pred. No. 2.8e-64; iive 0; Mismatches 150;
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                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                           Query Match 35.9
Best Local Similarity 72.4
Matches 417; Conservative
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nucleic

Run on:

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Q9y627 homo musculu
Q8y627 homo sapien
Q8cfg8 mus musculu
Q8crc5 homo sapien
Q9by77 homo sapien
Q9by77 homo sapien
Q9mias homo sapien
Q7c6n1 homo sapien
Q7c6n1 homo sapien
Q9tuc5 macaca mula
Q9tuc5 macaca mula
Q8tuc5 macaca mula
Q8tuc5 macaca mula
Q8tuc9 homo sapien
Q8tuc9 homo sapien
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Q8tuc9 musculu
Q8vh32 mus musculu
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Q8iwll homo sapien
Q91w8 homo sapien
Q9bcs8 homo sapien
Q9dc75 mus musculu
Q7t0t0 xenopus lae
Q8k4q8 mus musculu
Q8c979 mus musculu
                                                                                                                                                               Q863al bos taurus
Q91t06 ovis aries
Q91sq9 cyprinus ca
Q911x4 sus exrofa
Q9188 equus cabal
Q910g1 equus cabal
Q919q8 brachydanio
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O9xsq2 ovis aries
O9vet6 drosophila
Q86nz7 drosophila
                                                                                                          Q86yk9 homo sapien
Q8tcd8 homo sapien
Q9i9g7 carassius a
                              Q9z294 rattus sp.
Q7tmc0 rattus norv
                                                                   098ta4 gallus gall
057451 gallus gall
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Moduses T., Otta T., Tauber A.I., Sastry K.N.;
Modusacterization of two mannose-binding protein cDNAs from rhesus
monkey (Macaca milatta): structure and evolutionary implications.";
Glycobiology 6:543-550(1996).
RNBL; L43911; AAB48071.1; -.
HSSP; P11226; JHUP.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IFR008160; Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
Mannose-binding protein C (Fragment).
Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae;
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Q8C979
Q9Y6Z7
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09N1X3
08MJA5
09TUC5
08TC19
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Q9BWP8
Q9DC75
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Q8CF9B
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Q919Q9
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Q9CQ11
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O57451
Q86YK9
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Q86NZ7
                                    Q9Z294
Q7TMC0
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                                                                                                                                                       091907
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Q95L88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97031450; PubMed=8877375;
                                                                                                                                                                                                                                                                          29N0G1
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                                                                                                                                                                                                                                                                          Cercopithecinae; Macaca.
NCBI_TaxID=9544;
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-MODEL=frame+ 1-4D-model -DEV=xlp
-MODEL=frame+ 1-4D-model -DEV=xlp
-MODEL=frame+ 1-4D-model -DEV=xlp
-G-GROZ 1/USFTO spool p/US10054536/runat 18062004 173455 13584/app_query.fasta_1.903
-D=-CGROZ 1/USFTO spool p/US10054536/runat 18062004 173455 13584/app_query.fasta_1.903
-DS=SFTREMEL_25 -QFMT=fastan -SUFFIX=rspt"-MINMATCH=0.1 -IGOPECH=0 -IGOPEXT=0
-UNITS=bits -STRAT=1 -END=-1 -HAPRIXENE-blosum62 -TRANS=human40 cdi -LIST=45
-UNITS=bits -STRAT=1 -END=-1 -HAPRIXENE-Blosum62 -ALIGN=15 -MODE=LOCAL
-UNITS=bits -STRAT=1 -HEAPSIZE=50 -MINLEN=0 -MAXLEN=20000000
-USFR-US10054536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCPU=6 -ICPU=3
-UNITS-BITS -USIOS4536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCBU-6 -ICPU=3
-USFR-US10054536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCBU-6 -ICPU=3
-USFR-US10054536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCBU-6 -ICPU=3
-USFR-US10054536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCBU-6 -ICPU=3
-USFR-US10054536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCBU-6 -ICPU=3
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-USFR-US10054536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCBU-6 -ICPU=3
-USFR-US10054536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCBU-6 -ICPU=3
-USFR-US10054536 @CGN 1 1.86 @runat 18062004 173455 13584 -UCBU-6 -ICPU=3
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9522.913 Million cell updates/sec
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                                                                                                                                             June 18, 2004, 20:56:36; Search time 49.5 Seconds
                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                        - protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                           1017041 segs, 315518202 residues
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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Database

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Result

Minimum DB Maximum DB

Maximum

Searched:

Sequence:

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US-10-054-536-2 (1-747) x Q28517 (1-245)
                                                                                                                                                                                                          16 PO'
245 MAI
25693 MW; 1
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814.50
75.92%
63.27%
59.67%
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                                                    SEQUENCE FROM N.A.
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SIGNAL
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mannose-binding protein A precursor (Fragment).
Macaca mulatta (Rhesus macaque).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGICCCCTGCACCTCCCATCTGGCCGTCTGTGAGTTCCCTATC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 AA; 24911 MW; 449CBE887C89732E CRC64;
                                                                                                236
195
15
                                                                                              Length:
Matches:
Conservative:
Mismatches:
                                                                                                                               Indels:
LINTERPRO; IPR001304; Lectin C.

RE PERM; PP00139; Collagen; 1.

R PARAT; SM00034; CLECT; 1.

R PROSITE; PS00615; C TYPE LECTIN 1; 1.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

NON TER 1.
                                                                                                                                      Gaps:
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1073.00
97.22%
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                                                                                                           Percent Similarity:
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100 AlaLysLeuAlaAsnLeuGluArgGlnLeuGlnSerLeuArgSerGluLeuAspHisMet 119
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
NCBL_TaxID=9544;
                                                                                                                                                                                                                                                                             POTENTIAL.
MANNOSE-BINDING PROTEIN A.
AFAF0FCEF3DE6146 CRC64;
                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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79

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661 GATTGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCAT 720
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GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Liver;
MEDLINE-86196130; PubMed=3009480;
Drickamer K., Dordal M.S., Reynolds L.;
"Mannose-binding proteins isolated from rat liver contain
carbohydrate-recognition domains linked to collagenous tails. Complete primary structures and homology with pulmonary surfactant
                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10118;
                                                        241 AATCCAGGGCCTTCTGGGTCACCAGGACCAAAGGGCCAAAAAGGAGACCCTGGAAAAAGT
                                                                           80 SerproGlylleProGlyLeuProGlyLeuLysGlyGlnLysGlyAspSerGlylleAsp
                                                                                                                 CCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drickamer K., Dordal M.S., Reynolds L.;
Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF080607, AAC31936.1; -.
HSSP; P19999, 1RTM.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF01391; Collagen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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01-MAY-1999 (TrEMBLrel. 10, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mannose-binding protein (Fragment).
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J. Biol. Chem. 261:6878-6887(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  721 CIGGCCGICIGIGAGIICCCI 741
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                                                                    CTGACCTACACAAACTGGAACGAGGGTGAACCCAACAATGCTGGTTCTGATGAAGATTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agah A., Young K., Stahl G.L.; "Isolation, purification and cloning of a porcine mannose-binding
                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa (Pig).
Eukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria, Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AF164576; AAD45377.1; -.

HSSP; P11226; 1HUP.

GO; GO:000529; F:sugar binding; IEA.

GO; GO:0007157; P:heterophilic cell adhesion; IEA.

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; Clg helix.

InterPro; IPR008161; Clg helix.
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1161
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Matches:
Conservative:
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Indels:
                                                                                                                                                                                                                                                                            240 AA
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pfam; PP01391; Collagen; 2.
Pfam; PF000059; lectin. c; 1.
ProDom; PD000007; Clg.helix; 1.
SMART; SMO0034; CLECT; 1.
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808.00
74.90%
65.18%
59.19%
                                                                                                                                                                                                         ValCysGluPhePro 244
                                                                                                                                                                                        GTCTGTGAGTTCCCT 741
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                                                                                                                                                                                                                                                                            PRELIMINARY;
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Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE=Liver;
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SEQUENCE 240 A
                                                                                                                                                                                                                                                                                                                                                                                                           NCBL_TaxID=9823;
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Alignment Scores:
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ProProGlySerValGlyAlaProGlySerGlnGlyProLysGlyGlnLysGlyAspArg
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                                       44D790F8E12815A9 CRC64;
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136
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Last sequence update)
Last annotation update)
                                                             Length:
Matches:
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Pfam; PP00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                (1-224)
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                              NON TER 1 1 7 SEQUENCE 224 AA; 23800 MW;
                                                           3.87e-56
684.00
69.83%
58.62%
50.11%
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Q7TMC0;
Q7TMC0;
01-OCT-2003 (TEMBLRel, 25, C;
01-OCT-2003 (TEMBLRel, 25, L;
01-OCT-2003 (TEMBLRel, 25, L;
Ab2-011 (Ab2-001);
                                                                                                              x Q9Z294
                                                                                                              US-10-054-536-2 (1-747)
                                                                         Percent Similarity:
Best Local Similarity:
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117 AlaMetArgLysTrpValLeuLeuSerMetSerGluAsnValGlyLysLysFyrPheMet 136
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                                                                                                  SEQUENCE FROM N.A.

SUC.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,

Xu C.S., Li W.Q., Li Y.C., Han H.P., Wang G.P., Chai L.Q., Yuan J.Y.,

Yang K.J., Yan H.M., Chang C.F., Zhao L.F., Ma H., Wang L., Wang S.F.,

Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;

"Liver regeneration after PH.",

Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; A7225174; AAP92575.1;

EMBL; A7325178; AAP92579.1;

SEQUENCE 371 AA, 39978 MW; 774F06369D895A03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGTCCCTGTTTCCATCACTCCCTCTCCTTCTCTGAGTATGGTGGCGGCGTCTTACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAACCAGGCCAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA
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97 ValGluPheAspThrThrAsnIleAspLeuGluIleAlaAlaLeuArgSerGluLeuArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361 CGTATCAAAAGTGGCTGACCTTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTG
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Matches:
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636.00
72.60%
57.53%
46.59%
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Best Local Similarity:
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106 AspLeuHisArgGlnIleThrAspLeuGluAlaLysIleArg---ValLeuGluAspAsp 124
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SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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SEQUENCE FROM N.A.
STRAIN=White Leghorn; TISSUE=Liver;
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25645 MW;
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NON TER 238
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NCBI_TaxID=9031;
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                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
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GO; GO: 0005529; C:intracellular; IEA.
GO; GO: 0005529; F:sugar binding; IEA.
GO; GO: 00003700; P:transcription factor activity; IEA.
GO; GO: 0000355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000160; Cla delix.
InterPro; IPR001005; HTHARAC.
InterPro; IPR001005; HTHARAC.
InterPro; IPR00104; Lectin_C.
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ProDom; PE000007; Clg_helix; 1.
SWART; SW00034; CLECT; 1.
PROSITE; PS000415; C_TYPE_LECTIN_1; 1.
PROSITE; PS00041; TYPE_LECTIN_2; 1.
PROSITE; PS00041; HTH ARAC_FAMILY 1; 1.
    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence
01-OCT-2003 (TrEMBLrel. 25, Last annotatin
Mannose-binding lectin protein precursor.
Gallus gallus (Chicken)
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355 ATGGCACGTATCAAAAAGTGGCTGACCTTCTCTGGGCAAACAAGTTGGGAACAAGTTC 414
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205 TyrLeuSerGlyGlyProLeuThrTyrSerAsnTrpLysProGlyGluProAsnAsn---
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Eukaryota; Matazoa; Madata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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LysGlyGluArgGlyIleValValThrAspAspLeuHisArgGlnIleThrAspLeuGlu
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| AsnTrpLysProGlyGluProAsnAsn---HisLysAsnGluAspCysAlaValIleGlu
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-CCT-2003 (TrEMBLrel. 25, Last annotation update)
Surfactant, pulmonary-associated protein D.
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Pfam; PF01391; Collagen; 3.—
Pfam; PF00059; lectin c; 1.
SWART; SM00034; CLECT; 1.
PROSITE; PS00614; C.TYPE_LECTIN_1; 1.
PROSITE; PS50041; C.TYPE_LECTIN_2; 1.
SEQUENCE 375 AA; 37698 MW; 79380764F2B86E67 CRC64;
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26
26
20
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375
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(TrEMBLrel. 21, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Matches:
Conservative:
Mismatches:
Indels:
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454.00
55.07%
43.61%
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Best Local Similarity:
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Similarity:
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DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----CTGCAAACAGAAATGGCACGTATC 366
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149 AlabroGlyMetGlnGlySerAlaGlyAlaArgGlyLeuAlaGlyProLysGlyGluArg 168
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              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                   Strausbergs;
Strausbergs;
Strausbergs;
Strausbergs;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; BC022318; AA422318.1; ---
ROG; GO:0005529; F:sugar binding; IEA.

InterPro; IPR008161; Clg helix.
InterPro; IPR008161; Collagen.

R Pfam; PF01391; Collagen; 4.

R Pfam; PF00059; lectin_C; 1.

R ProDom; PD000007; Clg_helix; 1.

R RAMART; SM00034; CLECT; 1.

R PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

R PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

R PROSITE; PS10014; C_TYPE_LECTIN_2; 1.

R PROSITE; PS10014; C_TYPE_LECTIN_2; 1.

R PROSITE; PS10014; C_TYPE_LECTIN_2; 1.

R PROSITE; PS10014; C_TYPE_LECTIN_2; 1.
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82
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Matches:
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450.00
55.07%
43.17%
Hypothetical protein. Homo sapiens (Human).
                                                                                                              SEQUENCE FROM N.A. TISSUE=Lung;
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Best Local Similarity:
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WEDLINE=2045672; PubMed=11003389;

WEDLINE=2045672; PubMed=11003389;

Witved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;

Witved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;

The homologue of mannose-binding lectin in the carp family Cyprinidae

RT sexpressed at high lavel in spleen, and the deduced primary

RT structure predicts affinity for galactose.";

Immunogenetics 51:55-964 (2000).

REMBL, AP227739; AAF63470.1; -.

REMBL, AP227739; AAF63470.1; -.

RO GO:000529; Resugar binding; IEA.

RO, GO:000529; P:stegar binding; IEA.

RICEPPO: IPR001304; Loctin_C.

RICEPPO: IPR001304; Loctin_C.

REMBL; REMBL; REMOSS4; LIECTIN_C.

REMBL; REMOSS4; LIECTIN_C.

REMBL; REMOSS4; LIECTIN_C.

REMBL; REMOSS5; REME LECTIN_Z.

REMBL; REMOSS4; LIECTIN_C.

REMBL; REMOSS5; REME LECTIN_Z.

REMBL; REMOSS5; REMEDIAN_Z.

REMBL; REMOSSTER; REMOSS5; C. TYPE_LECTIN_Z.

REMSTIRE REMOSSTER; REMOSS5; REMEDIAN_Z.

REMSTIRE REMOSSTER; REMOSS5; REMEDIAN_Z.

REMSTIRE REMOSSTER; REMEDIAN_Z.

REMBL; REMSTER REMEDIAN_Z.

REMBL; REMOSSTER; REMEDIAN_Z.

REMBL; REMOSSTER; REMEDIAN_Z.

REMBL; REMOSSTER; REMEDIAN_Z.

REMBL; REMOSSTER; REMEDIAN_Z.

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                                658 GAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MBL.
Carassius auratus (Goldfish).
Carassius auratus (Goldfish).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Carassius.
NCBI_TaxID=7957;
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Last annotation update)
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2003 (TrEMBLrel. 25, Last annotation update
Mannose binding-like lectin precursor (Fragment).
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37.71%
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TISSUE=Liver;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCAACAATGCTGGTTCTGATGAAGATTGTGTATTGCTACTGAAAAATGGCCAGTGGAAT 696
ProGlyThrAlaGlyGluLysGlyGluArgGlyProSerGlyProGlnGlySerProGly
                                                                        92 SerGluSerValleuGluSer----LeuLysSerGluIleGlnGlnCuLysAlaLys
                                                                                                                              355 AIGGCACGTATCAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTC
                                                                                                                                                                                                                                             ::::::||||:::|||| :::
130 TyrileThrAspGlyValValGlyAsnPheAspGlnGlyLeuLysSerCysMetGluPhe
                                                                                                                                                                                                                                                                                                        475 CAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGCAGTTTGTGGATCTGACAGGAAATAGACTGACCTACACAAACTGGAACGAGGGTGAA
                                               110 ProAspAspTyrLysGlyLeuGlnAspCysGlyVallleGluAspThrGlyLeuTrpAsp
                                                                                                                                                                                                                                                                                                                                                                                              -----AAGGAGGAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Bovine surfactant protein D. Genomic characterization, chromosomal localization and tissue distribution.";

EMBL, AJ548849, CAD69922.1;

EMBL, AJ548849, CAD69922.1;

EMBL, AJ548849, CAD69922.1;

EMBL, AJ548849, CAD69922.1;

JOINED.

GO, GO:0005529, F:sugar binding; IEA.

InterPro; IPR0018160, Collagen.

InterPro; IPR00184, Lectin.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACGTCCCCTGCTCCACCTCCCATCTGGCGTCCCTATC 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     surfactant protein D.
surfactant protein D.
4A74B7593508AE5D CRC64;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Surfactant protein D precursor.
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Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS006615; C TYPE_LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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369 AA;
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SIGNAL
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Q863A1
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369

Length:

2.92e-31

Alignment Scores:

Pred. No.:

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165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365
                                                                                                                                                             235 CCAGGAAATCCAGGGCCTTCTGGGTCACCAAGGACCAAAAGGGACAAAAAGGAGACCCTGGA
                                                                                                                                                                                                                                                                                                                                                                                                              ------GCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCACGTATCAAAAAGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                 GlylleLeuGluGlyGlnLeuGlnArgLeuGlnAsnAlaPheSerGlnTyrLySLysAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 LysThrPheGlnAspAlaGlnGlnIleCysThrGlnAlaGlyGlyGlnLeuProSerPro
                                                                                                                                                                                                                                                                                                                                                               ::: ||| ||| ||| ||| 246 MetLeuPheProAsnGlyArgSerValGlyGlubys11ePheLysThrGluGlySerGlu
                                                                                                                                                                                                       GGGGAACCAGGC----CAAGGGCTCAGAGGCTTACAGGGCCCCCCTGGAAAGTTGGGGCCCT
                                                                                                                                                                                                                                                                                                      186 GlnGlyProSerGlyAlaArgGlyProProGlyLeuLysGlyAspArgGlyThrProGly
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Dulmonary surfactant protein A (Pulmonary surfactant-associated protein A).
SPAS OR SP-A.
Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Cetartiodactyla; Ruminantia; Pecora, Bovoidea;
NOGH_TAXID=9940;
   88
330
89
117
                 Conservative:
Mismatches:
Indels:
 Matches:
                                                                                                                                                                                                                                                                                                                                            ---AAAAGTCCGGATGGTGATAGTAGCCTGGCT
                                                                                                   x Q863A1 (1-369)
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422.50
52.68%
39.29%
30.95%
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          Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                  US-10-054-536-2 (1-747)
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SEQUENCE FROM N.A.
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663

723

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MEDLINE=20456722; PubMed=11003389;
Witved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;
Vitved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;
Witved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;
Witved L., Holmskov U., Koch C., Teisner B., Hansen S., Skjodt K.;
structure at high level in spleen, and the deduced primary
structure predicts affinity for galactose.";
Immunoapenetics 51:955-964(2000).
EMBL: AF227737; AAF65468.1;
HSSP, P35247; 1808.
                      165 ProArgSerProGludludsnGludlalleThrSerIleValLysLysHisAsnThrTyr
                                                     544 GCCTTCCTGGGCATCACTGATGAGAGAGAGAGAGGCAGTTTGTGGATCTGACAGGAAAT
                                                                          604 AGACTGACCTACACAAACTGGAACGAGGTGAACCCAACAATGCTGGTTCTGATGAAGAT
                                                                                                                                            ProvalAsnTyrThrAsnTrpTyrProdlyGluProArgGlyArgGlyLys---GluLys
                                                                                                                                                                       TGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTG
                                                                                                                                                                                             Cyprinus carpio (Common carp).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Ostariophysi; Cypriniformes;
Cyprinidae; Cyprinus.
NCBI_TaxID=7962;
CCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATCAAGGAGGAA-
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MANNOSE BINDING-LIKE LECTIN.
S -> T.
D019291D1167730D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005529; Fsugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR008160; Collagen.
InterPro; IPR001391; Lectin_C.
Pfam; PF001391; Collagen; 2.
Pfam; PF00059; lectin_C; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Matches:
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01-0CT-2000 (TrEMBLrel. 15, Last seque
01-0CT-2003 (TrEMBLrel. 25, Last annot
Mannose binding-like lectin precursor.
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244 AlaileCysGluphe 248
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418.50
54.05%
36.68%
30.66%
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256
235
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ::: |||:: :::|||
145 SerLeuAsnPheAspAlaIleLysGluLeuCysAlaArgAlaGlyGlyHisIleAlaAla 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAAGGAGACCCTGGA---AAAAGTCCGGATGGTGATAGTAGCTGGCTGCCTCAGAAAGA 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ||||||||:::||||||| ::: ||| |||
LysGlyGluProGlyGluArgGlyProProGlyPheProAlaTyrLeuAspGluGlu--- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- AAACAAGTTGGGAACAAGTTCTTCCTGACCAATGGTGAA 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 LeulleLeuGlnGlySerMetLeuGluValGlyGluLysValPheSerThrAsnGlyGln 144
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                                                                                                                                                                       SP-B, and SP-C: isolation
          MEDLINE=20215262; PubMed=10749753; Braems G.A., Yao L.-J., Inchley K., Brickenden A., Han V.K.M., Grolla A., Challis J.R.G., Possanayer F.; Grolla A., Challis J.R.G., Possanayer F.; and interant protein cDNAs: use in studies on fetal lung sand maturation after prolonged hypoxemia."; Am. J. Physiol. 278:L754-L764(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00615; C_TYPE LECTIN 1; 1.
PROSITE; PS0041; C_TYPE_LECTIN_2; 1.
SEQUENCE 248 AA; 26394 MW; D65E7293BBFF1FD9 CRC64;
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102
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                                                                                                                                                           Pietschmann S.M., Pison U.;
"cDNA cloning of ovine pulmonary SP-A, SP-
two different sequences for SP-B.";
Am. J. Physiol. 278:1765-1178 (2000).
EMBL; AF211856; AAF18995.1;
EMBL; AF076633; AAF31148.1;
GO GO:0005529; E:sugar binding; IEA.
InterPro; IPR001806; Collagen.
InterPro; IPR001304; Lectin_C.
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                                                                                        Am. J. Physiol. 278:L754-L764(2000)
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TISSUENCE FROM N.A.
TISSUE=Lung;
MEDLINE=20215263; PubMed=10749754;
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 TCAGAAACTGTGACCTGTGAGGATGCCCAAAAGACCTGCCCTGCAGTGATTGCCTGT--- 114
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114 GlnGlnLeuLysAlaLysIleAlaThrPheGluLysValAlaSerValGlyHisPheArg 133
                     LeuAsp------GlyAladluProGlnAsnLeuAsnCysproAlaTyrGlyGlyValPro 38
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                                                                                                                                                                                                                                                                                                                                                                    GCCATTCAGAATCTCATC-------AAGGAGGAAGCCTTCCTGGGCATC 558
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|AlaLeuLeuLyBLeuValValSerSerGlyLeuSerSerLySLysBroTyrIleGlyVal 193
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214 AsnTrpGlyProGlyGlnProAspAspTyrLysGlyLeuGlnAspCysGlyVallleGlu 233
                                                                                                        59 IleGlyProLysGlyGlwLysGlyGlwSerGlyVal-----SerValGlnGlyPro
                                                                                                                                                                                 277 CAAAAAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGTCTTGGCTGCTCAGAAAGA
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| ProGlyLysAlaGlyProProGlyProAlaGlyGluLysGlyGluArgGlyProThrGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Porcine Lung Surfactant Protein D (SP-D): cDNA cloning, chromosomal localisation and tissue distribution.";
J. Immunol. 164:1442-1450(2000).
BMBL; AR122496; AAF22145.2;
HSSP; P35247; 1B08.
GO; GO:0005529; F:sugar binding; IEA.
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MEDLINE=20109098; PubMed=10640760;
Van Eil, M., Haagsman H.P., Skinner T., Archibald A.L., Reid K.B.M.,
Lawson P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         679 AAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCCATCTGGCCGTCTGTGAG
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                            115 AGCTCTCCAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGAT-
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Lung surfactant protein D precursor.
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|||| GlyGluThrGlyFroLysGlyGluValGlyAlaLeuGlyMetGlnGlySerThrGlyAla 158
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| GİYProProGİYLeuLysGIYBAFGGIYProProGIYGluArgGIYAlaLysGIYGIU 218
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Matches:
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                                                                                                                                                                      POTENTIAL
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Collagen; Signal. 20 POTENTIA!
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InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR001304; Lectin_C.
Pfam; PF001391; Collagen; 3.
Pfam; PF001609; lectin_c; 1.
ProDom; PD000007; Clg_helix; 2.
SMART; SM00034; CLECT; 1.
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 CAAGTIGGGAACAAGTICTICCIGACCAAIGGIGAAAIAAIGACCITIGAAAAAGIGAAG 456
                                                                                                                                               517 GCCATTCAGAATCTCATC-----AAGGAGGAAGCATCCTGGGCATCACTGATGAG 567
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|LeuThrLeuThrLeuIleLeuLeuAlaValSerGlyThr---LysCys---AspValLys
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                                                                                                                                                                259 GlyvaldlygluLysllepheLysThrdlyglyPheGluLysThrPheGlnAspAlaGln
                                                                                           GCCTTGTGTGTCCAAGTTCCAGGCCTCTGTGGCCACCCCCAGGAATGCTGCAGAATGGA
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Mammalia, Butheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Weber B.I.L., Hospes R., Gortner L.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
REMBL, AF4000580; AALOT690.1;
CGO; GO: 00005529; F: Sugar binding: IEA.
RICETPO: IPR008160; Collagen.
RICETPO: IPR001304; Lectin_C.
R Pfam; PF001391; Collagen, 2.
R Pfam; PF00059; Lectin_C; 1.
R RPART; SM00034; CLECT; 1.
R PROSITE; PS00615; C TYPE_LECTIN_1; 1.
R PROSITE; PS50041; C TYPE_LECTIN_2; 1.
SMART; CARBA; Z6047 MW; B71133E005C9A5C1 CRC64;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence of 01-OCT-2003 (TrEMBLrel. 25, Last annotation Pulmonary surfactant-associated protein A.
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| 111 LeuHisAsplleArgHisGlnIleLeuGlnLeuMetGlyAlaLeuSerLeuGlnGlySer
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Sequence 2, Application US/09198603C

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Sequence 2, Application US/09198603C

APPLICANT: TULLY, Raymond E. APPLICANT: TULLY, Raymond E. APPLICANT: MONING, Michael T. TITLE OF INVENTION: EXPRESSION OF MANNOSE-BINDING PROTEIN IN METHYLOTROPHIC TITLE OF INVENTION: YEAST

FILE REFERENCE: A7290

FILE REFERENCE: A7290

CURRENT APPLICATION UNDER: US/09/198,603C

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 26
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Sequence 4, Appli
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ORGANISM: Human
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Query Match: DB: TR-10-054-536-2 (1-747)	118	Db 126 AlaProGlyI	Oy 178 GGGBACCAG	143	163	Qy 286 GACCCTGGAA	328	Oy 367 AAAAAGTGGG	Db 223 LysLysAlav	Qy 427 GGTGAAATAI     :::  Db 243 G1yAlaVali	Qy 487 GCCACCCCC       :::    Db 263 AlaSerPro	538	598	Db 303 GlyGluile	652	Db 323 GlnProGlu	Qy 712 ACCTCCCAT Db 343 LysGlnLeu RESULT 3 US-09-029-156-1 ; Sequence 1, Applicati ; Patent No. 636534: ; Patent INFORMATION:	APPLICANT: WAKAMI TITLE OF INVENTION TITLE OF INVENTION TITLE OF SEQUENCE CORRESPONDENCE ADD CORRESPONDENCE ADD CORRESPONDENCE ADD STREET: 233 SOU STREET: Chicago STATE: Illinois COUNTRY: United	
61 GAAACTGTGACGGTGGCCAAAAGACCTGCCCTGCAGTGATTGCCTGTAGCTCT 120 			181 GAACCAGGCCTAAGGCTTACAGGCCCCCCTGGAAAGTTGGGGCCTCCAGGA 240			301 CCGGATGGTGATAGCCTGGCTGCCTCAGAAAGAAAAGCTCTGCAAACAGAAATGGCA 360 	361 CGTATCAAAAGTGGCTGACCTTCTCTGGCCAAACAAGTTGGGACAAGTTCTTCTG 420	ACCAATGGTGAAATAATGACCTTTGAAAAGTGAAGGCCTTGTGTGTG			541 GAAGCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGA 600 	601 AATAGACTGACCTACACAAACTGGAACGAGGGTGAACCCAAGATGCTGGTTCTGATGAA 660 	661 GATTGTGTATTGCTACTGAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCCAT 720	221 AspCysValLeuLeuLeuLysAsnGlyGlnTrpAsnAspValProCysSerThrSerHis 240	721 CTGGCCGTCTGTGGATTCCCTATC 744	4	BESULT 2 US-09-011-735-1 ; Sequence 1, Application US/09011735B ; Patent No. 6110708 ; GENERAL INFORMATION: ; APPLICANT: Wakamiya, No. 6110708utaka ; TITLE OF INVENTION: Recombinant Conglutinin and Producing Method Thereof ; FILE REFERENCE: 19036/3454B ; CURRENT APPLICATION NUMBER: US/09/011,735B	; CURRENT FILING DATE: 1998-05-22 ; EARLIER APPLICATION NUMBER: UP 7-209698 ; EARLIER FILING DATE: 1995-08-17 ; NUMBER OF SEQ ID NOS: 6 ; SOFTWARE: PatentIN Ver. 2.0 ; SEQ ID NO 1 ; LENGTH: 351 ; TYPE: PRT: TYPE: PRT: CONTINENT CONTINEN	Alignment Scores: 1.15e-36 Length: 351  Pred. No.: 442.50 Matches: 91 Score: 56.77% Conservative: 39 Percent Similarity: 39.74% Mismatches: 74
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323 GlnProGluAsnCysValGluIlePheProAspGlyLysTrpAsnAspValProCysSer 342
    283 LysAsnAlaTyrLeuSerMetAsnAspIleSerThrGluGlyArgPheThrTyrProThr 302
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                                 469 AAGTICCAGGCCICTGIGGCCACCCCCAGGAAIGCIGCAGAAIGGAGCCAIICAGAAI
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; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID; IMMUNOGLOBULINS
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 43
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-194
PRIOR APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
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359.00
74.07$
61.11$
26.30$
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                                                                                                                                                                                                                                                ;Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match:
                                                                                                                                                                                                                 RESULT 4
5514582-16
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|GlyalaProGlyGluThrGlyAlaProGlyArgAlaGlyValThrGlyProSerGlyAla 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAAGTGGCTGACCTTCTCTCTGGGCAAACAAGTTGGGAACAAGTTCTTCCTGACCAAT 426
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Patentin Release #1.0, Version #1.30
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 19036/34546
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                  FILING DATE:
APPLICATION NUMBER: PCT/JP95/02035
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JPA - 209698
FILING DATE: 17-AUG-1995
ATTORNEY AGENT INFORMATION:
           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,156
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP96/00173
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                                                                                                                                                                                                             NAME: Gass, David A. REGISTRATION NUMBER: 38,153
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442.50
56.77$
39.74$
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Best Local Similarity:
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Query Match:
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: WAkamiya, No. 6110708utaka
TITLE OF INVENTION: Recombinant Conglutinin and Producing Method Thereof
FILE REFERENCE: 19036/34548
CURRENT APPLICATION NUMBER: US/09/011,735B
CURRENT FILING DATE: 1998-05-22
EARLIER APPLICATION NUMBER: JP 7-209698
EARLIER FILING DATE: 1995-08-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
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61 TyrValThrGlyGlyArgLeuThrTyrSerAsnTrpLysLysAspGluProAsnAspHis
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66
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;Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.
; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
;IMMUNOGLOBULINS
                                                                                                                                                                                                                                                                                                                                                                    Matches:
Conservative:
Mismatches:
Indels:
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                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,670
FILING DATE: 21-JAN-1994
PRIOR APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
APPLICATION NUMBER: 808,122
APPLICATION NUMBER: 440,625
FILING DATE: 16-DEC-1991
APPLICATION NUMBER: 315,015
FILING DATE: 22-NOV-1989
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347.50
73.15%
61.11%
25.46%
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Best Local Similarity:
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ORGANISM: Bovine
                                                                                                                                                                                                                                                                                            LENGTH: 107
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337 AAAGCTCTGCAAACAGAAATGGCACGTATCAAAAGTGGCTGACCTTCTCTCTGGGCAAA 396
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5514582-20
; PATENT NO. 5514582
; PATENT CAPON, DANIEL J.; LASKY, LAURENCE A.
TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID
; IMMUNOGLOBULINS
; VURBENT APPLICATION DATA;
; APPLICATION NUMBER: US/08/185,670
; FILING DATE: 21-JAN-1994
; PRIOR APPLICATION NUMBER: 986,931
; FILING DATE: 08-DEC-1992
; FILING DATE: 16-DEC-1991
; FILING DATE: 16-DEC-1991
; APPLICATION NUMBER: 440,625
; FILING DATE: 22-NOV-1989
                                                                                                      is a protein-constituting amino
                                                                                                                                                                              Xaa is a protein-constituting amino
                                  is a protein-constituting amino
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                 ; LOCATION: (6)
; OTHER INFORMATION: Xaa is a
US-09-011-735-6
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61.15%
38.85%
20.99%
                                  OTHER INFORMATION: Xaa
                                                                                                        OTHER INFORMATION: Xaa
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                                                                                                                                                             LOCATION: (5)
OTHER INFORMATION:
VARIANT
                                                                                                                                            NAME/KEY: VARIANT
                                                                                                                                                                                                                  NAME/KEY: VARIANT
                                                                    NAME/KEY: VARIANT
LOCATION: (3)
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity
                                                                                                                                                                                                                                                                                                           Alignment Scores:
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28 LysAlaArgLysHisSerLysArgArgValArgAspLysAspGlyAspLeuLysThrGln 47
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-365-103B-4; Sequence 4, Application US/08365103B; Patent No. 5766943
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BER: Uirf
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NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirl
TELECOMMUNICATION INFORMATION:
TELEPAX: (515) 288-1338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, MC
STREET: 801 Grand Ave
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                     Sequence 99, Application US/09602877A

Sequence 99, Application US/09602877A

Patent No. 6432707

SERERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Viangchun

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: COMPOSITIONS OF BREAST CANCER

FILE REFERENCE: 210121.446C5

CURRENT APPLICANT: US/09/602,877A

CURRENT FILING DATE: 2000-06-22

NUMBER OF SEQ ID NOS: 107

SOFTWARE FEASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     271 AAGGGCCAAAAAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGCCTG--
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100 AspLysAsnCysLeuGlnTyrArgLeuValIleCys 111
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Matches:
Conservative:
Mismatches:
Indels:
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Matches:
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APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
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56.25%
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Best Local Similarity:
Query Match:
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Percent Similarity:
                                                 LENGIH: 111
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                                    SEQ ID NO:20
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355 ATGGCACGIATCAAAAAGTGGCTGACCTTCTCTGGGCAAACAAGTTGGGAACAAGTTC 414
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APPLICANT: Nunez, Raphael D.
APPLICANT: Yodoi, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
WUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEE: Zarley, McKee, Thomte, Voorhees & Sease: 801 Grand Ave. Suite 3200
Des Moines
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
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TOPOLOGY: linear
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Query Match:
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128 ValAlaLysLeuTrplleGluIleLeuIleSerLysGlyThrAlaCysAsnIleCysPro 147
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257 ArgSerTyrLeuAspAlaTrpValCysGluGlnLeuAlaThrCysGlu 272
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APPLICANT: Wunez, Raphael D.
APPLICANT: Yodoi, Jungi
TITLE OF INVENTION: DNA Sequences for Soluble Froms of CD23
TITLE OF INVENTION: and Methods of Use for Same
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease STREET: 801 Grand Ave. Suite 3200 CITY: Des Moines STATE: lowa
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
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MOLECULE TYPE: protein
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Percent Similarity:
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121 SerbeuglyLeuAsndluLysArgThrAlaSerAspSerbeugluLysbeuglnGludlu 140
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141 ValàlaLysLeuTrplleGluIleLeuIleSerLysGlyThràlaCysAsnIleCysPro 160
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270 ArgSerTyrLeuAspAlaTrpValCysGluGlnLeuAlaThrCysGlu 285
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Patent No. 5766943
GENERAL INFORMATION:
APPLICANT: Lynch, Richard G
APPLICANT: Vodos, Jungi, Raphael D.
APPLICANT: Yodos, Jungi, TILL OF INVENTION: DNA Sequences for Soluble Froms of CD23
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 AGCCTGCCTCAGAAAGAAAGCT-----
                  FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
ATTORNEY, AGENT TINRORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Uirf N5-24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 288-367
INPORMATION FOR ESD ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels:
UMBER: US/08/365,103B
28-DEC-1994
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179 GlnTrpile------
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      APPLICATION NUMBER:
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Best Local Similarity:
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Pred. No.:
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277 GlyGlnGlyGluAspCysValMetMetArgGlySerGlyGlnTrpAsnAspAlaPheCys 296
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Mismatches:
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Matches:
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; Sequence 20, Application US/09535521
; Patent No. 6410714
; GENERAL INFORMATION:
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196.50
44.35%
29.13%
14.40%
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US-09-535-521-20
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Query Match:
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168 ValAlaLysLeuTrpIleGluIleLeuIleSerLysGlyThrAlaCysAsnIleCysPro 187
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                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/365,103B
FILING DATE: 28-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
    FITLE OF INVENTION: and Methods of Use for Same
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                                         E: Zarley, McKee, Thomte,
801 Grand Ave. Suite 3200
                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               REPERENCE DOCKET NUMBER: UIF TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 288-3667 TELEPAX: (515) 288-1338 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 327 amino acids
                                                                                                                                                                                                                                                                       37,719
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201.50
46.59%
28.98%
14.76%
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NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,7
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                                                                                Iowa
: United States
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                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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                                                                                             COUNTRY:
                                                                                STATE:
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369 |||::: | | | SerIleHisSerGlnGluGlnAspPheLeuAlaArgTyrAlaAsnLysLysGly 138 603 275 GCCAAAAAGGAGACCCTGGAAAAAGTCCGGATGGTGATAGTAGCCTGGCTGCCTCAGAAA 334 370 ---AAGIGGCIGACCIICICICIGGGCAAACAAGIIGGGAACAAGIICIICCIGACCAAI 426 487 GCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC---AAGGAGGAA 543 122 CAGGCATCAACGGCTTCCCAGGCAAAGATGGGCGTGATGGCACCAAGGGAGAAAAGGGGG 181 22 MetLysAlaGlnAspSerGluLeuSerGlnAsnLeuAspAlaLeuArgSerAspLeuAsn 41 42 AsnLeuLysSerGlnSerLeuAsnGluArgSerThrAlaLeu---HisSerLeuGluArg 60 84 APPLICANT: Weber, Stric R.
APPLICANT: Weber, Catherine A.
APPLICANT: Weber, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 19E RECEPTOR (CANINE CD23)
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 19E RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REFERENCE: AL-5
CURRENT APPLICATION NUMBER: US/99/535,521
CURRENT FILING DATE: 2000-03-24
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VEY. 2.1
SEQ ID NO 20 218 ---CTGGAAAGTTGGGGCCTCCAGGAAATCCAGGGCCTTCTGGGTCACCAGGACCAAAGG -------GluLeuHisValSerAsnGlySerGluCysAsnThrCysPro -GCTTACAGGGCCCCC----544 GCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAAT 4 GinAlaAlaGlnValSerGinAspMetLysGluIleGlnAla-----GluGlnLysArg ----ArgLysCysTyrTyrPheGly GAAAAGCTCTGCAAACAGAAATGGCACGTATCAAA--------297 ArgSerTyrLeuAspAlaTrpValCysGluGlnLeuAlaThrCysGlu -TCCCATCTGGCCGTCTGTGAG

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US-09-535-521-5
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Sequence 2, Application US/0953521

Setent No. 6410714

GENERAL INFORMATION:

APPLICANT: Weber, Eric R.

APPLICANT: McCall, Catherine A.

TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 1GE RECEPTOR (CANINE CD23)

TITLE OF INVENTION: NUMBER: US/09/535,521

CURRENT APPLICATION NUMBER: US/09/535,521

CURRENT FILING DATE: 2000-03-24

EARLIER FILING DATE: 1999-03-24

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2
                     717
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|GlnAlaAlaGlnValSerGlnAspMetLysGluIleGlnAla-----GluGlnLysArg 105
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MetlysalaGlnaspSerGluLeuSerGlnasnLeuaspAlaLeuargSeraspLeuasn 125
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Matches:
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Best Local Similarity:
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US-09-535-521-2
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263 CysValMetMetGlnGlySerGlyGlnTrpAsnAspAlaPheCysGlySerSerLeuAsp 282
GCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC---AAGGAGGAA 543
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88 GlnAlaAlaGlnValSerGlnAspMetLysGluIleGlnAla-----GluGlnLysArg 105
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APPLICANT: Weber, Eric R.
APPLICANT: Wecall, Catherine A.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY 19E RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
FILE REPERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT APPLICATION NUMBER: 60/125,913
EARLIER APPLICATION NUMBER: 60/125,913
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 292
                                     544 GCCTTCCTGGGCATCACTGATGAGAAGACAGAAGGGCAGTTTGTGGATCTGACAGGAAAT
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US-09-535-521-5
US-09-535-521-5
Sequence 5, Application US/09535521
Patent No. 6410714
GENERAL INFORMATION
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83 TrplleGlnAlaArgPheAlaCysSerLysLeuGlnGlyArgLeuAlaSerlleHisSer 102

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Sequence 17, Application US/09535521
Sequence 17, Application US/09535521
Fatent No. 6410714
GENURAL INFORMATION:
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL CANINE LOW AFFINITY IGE RECEPTOR (CANINE CD23)
TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES AND USES THEREOF
TITLE REPERENCE: AL-5
CURRENT APPLICATION NUMBER: US/09/535,521
CURRENT FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-03-24
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 17
LENGTH: 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              310 GATAGTAGCCTGGCTGCCTCAGAAAGGTCTGGCAAACAGAAATGGCACGTATC--- 366
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            --ArglysCysTyrTyrPheGly 182
                                                                                                                 GCCACCCCCAGGAATGCTGCAGAGAATGGAGCCATTCAGAATCTCATC----AAGGAGGAA 543
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|AlaSerIleHisSerGlnGluGluGlnAspPheLeuAlaArgTyrAlaAsnLysLysGly 222
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263 CysValMetMetGlnGlySerGlyGlnTrpAsnAspAlaPheCysGlySerSerLeuAsp 282
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                                               GGTGAAATAATGACCTTTGAAAAAGTGAAGGCCTTGTGTGTCTAAGTTCCAGGCCTCTGTG
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                                                                       TGTGTATTGCTACTGAAAAATGGCCAGTGGAATGACGTCCCCTGCTCCACCTCC----
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               169 GluLysTrpLeuAsnPheGln-
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Percent Similarity:
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Query Match:
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502 GCTGCAGAGAATGGAGCCATTCAGAATCTCATC---AAGGAGGAAGCCTTCCTGGGCATC
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